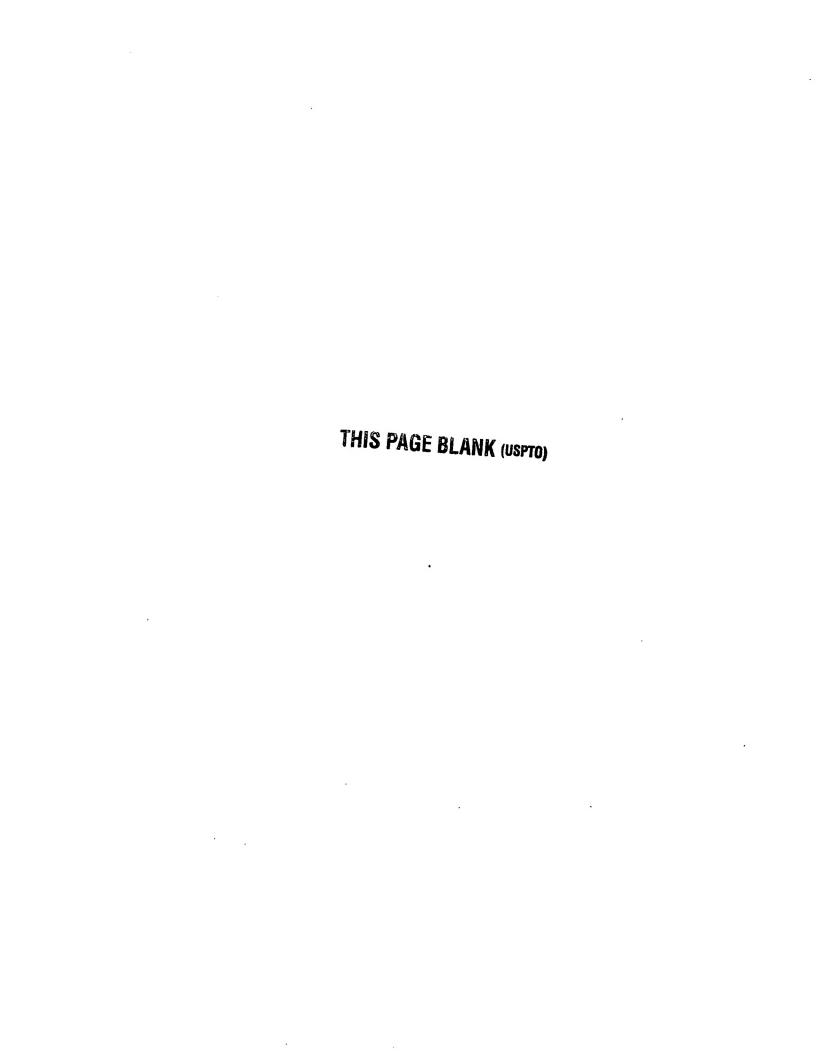
Access DB# 44436

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name:			E:	xaminer # :	Date:		
Art Unit:	Phone Nun	nber 30		Serial Number:			
Mail Box and Bldg/Room	Location:		_ Results	Format Preferred (circle):	PAPER	DISK	E-MAIL
if more than one search *******	is submitte ******	ed, please p	rioritize s	earches in order of ne	ed. ******	*****	*****
Please provide a detailed statem Include the elected species or st utility of the invention. Define known. Please attach a copy of	ructures, keyw any terms that	vords, synonym t may have a sp	s, acronyms ecial meani	s, and registry numbers, and c ng. Give examples or relevan	ombine wit	h the cor	ncept or
Title of Invention:							
Inventors (please provide full							
Earliest Priority Filing Da							
For Sequence Searches Only F appropriate serial number.	lease include a	ill pertinent infor	mation (par	ent, child, divisional, or issued p	atent numbe	ers) along	with the
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STAFF USE ONLY	******	Type of Searc	**************************************	Vendors and cost v	where appl	icable	
Searcher: 1604 Port	· · ·	Type of Searc	"· /	STN			
Searcher Phone #: 301-3	534_	AA Sequence (#)_		Dialog		<u> </u>	
Searcher Location:				Questel/Orbit			
Date Searcher Picked Up:	<u>/ </u>	Bibliographic		Dr.Link			
Date Completed:	<u> </u>	Litigation		Sequence Systems			
Clerical Prep Time:		Patent Family _		www/Internet			
		Other		Other (enecify)			

PTO-1590 (1-2000)



Run on: OM protèin - protein search, using sw model June 11, 2001, 16:22:00 ; Search time 18.58 Seconds (without alignments) 1546.081 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Title:
Perfect score:
Sequence: US-09-464-039-7 2139

1 MLPNTGRLAGCTVFITGASR......GNMALAIKLEKLMNQMNARL 418

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 198801 segs, 68722935 residues

.Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_67:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23	2 2	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	o	₅	4	ω	2	_	NO.	Result
2.0.5	217	217	218.5	218.5	221	222	222.5	222.5	223	224	224.5	227	231	232	233.5	235	235	236	237	241	244	256	267	286	665	708	891.5	1034	Score	
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200	261	256	251	246	248	253	320	271	275	285	301	679	894	278	255	266	246	736	258	246	240	238	248	436	282	274	293	938	Length	
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oxidoreductase (im	glucose 1-dehydrog	hypothetical prote	oxidoreductase, sh	0	hypothetical prote	probable short-cha	3-oxoacyl-[acyl-ca		probable sterol de	probable 3-oxoacyl	hypothetical prote	probable oxidoredu	multifunctional be		hypothetical prote	probable short-cha	3-oxoacyl-(acyl-ca		glucose 1-dehydrog		3-oxoacyl-[acyl-ca	probable 3-oxoacyl	Ω	•	hypothetical prote	н		cal pro	Description	

44	Δ. ω	42	41	40	39	38	37	36	35	34	33	32	31	30
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.9.6	o	9.6	9.6	9.6	9.6	9.7	9.7	9.8	9.9	9.9	9.9	9.9	10.0	10.0
253	319	255	592	256	250	286	265	285	900	279	241	735	284	246
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probable dehydroge	3-oxoacyl-[acyl-ca	2,5-dichloro-2,5-c	probable ephD prot	3-hydroxybutyrate	probable dehydroge	alcohol dehydrogen	probable short cha	short-chain dehydr	bifunctional beta-	hypothetical prote	(R,R)-butanediol d	multifunctional be	hypothetical prote	3-oxoacyl-(acyl-ca

ALIGNMENTS

RESULT 1 T34105 hypothetical protein C17G10.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T34105 R;Johnson, D. Submitted to the EMBL Data Library, June 1995 A;Description: The sequence of C. elegans cosmid C17G10. A;Reference number: 221476 A;Reference number: 221476 A;Reference number: 21476 A;Reterence number: 21476 A;Reterence number: 21476 A;Reference number: 214705 A;Residues: 1-938 < JOH> A;Residues: 25/1: 67/2: 158/3; 214/3; 329/3; 386/2; 465/3; 510/1; 525/2; 582/3; 709/1; A;Introns: 25/1: 67/2; 158/3; 214/3; 329/3; 386/2; 465/3; 510/1; 525/2; 582/3; 709/1;
RESULT 1 T34105 Typothetical protein C17G10.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T34105 R;Johnson, D. Submitted to the EMBL Data Library, June 1995 A;Description: The sequence of C. elegans cosmid C17G10. A;Reference number: Z21476 A;Reference number: Z21476 A;Reference number: Z1476 A;

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A;Resadues: 1-274 <570>
A;Croas-references: GB:AE004715; GB:AE004091;
A;Experimental source: strain PAO1
C;Genetics:
                                                                                                                            C;Accession: G83284
C;Accession: G83284
R;Stover, C.K.; Pham, X.Q.; Erwin,
Adman, S.; Yuan, Y.; Brody, L.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Map position: 5
A:Introns: 9/2; 66/3
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-293 <WIL>
A; Cross references: EMBL: 274029; PIDN: CAA98431.1;
A; Cross references: clone C45B11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein C45B11.3 - Caenorhabditis C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1 C;Accession: T19954
R;McMurray, A.
                                                                          A; Reference number: A82950; A; Accession: G83284
                                                                                                                                                                         probable short-chain dehydrogenase PA2892 [imported] - Pseudomonas
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-
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                                                             A; Status: preliminary
                                                                                                 A; Title: Complete genome
                                                                                                              .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
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                                                                                     sequence of Pseudomonas 50; MUID:20437337
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                                                                                                                                    Mizoguchi, S.D.
r, S.N.; Folger,
                       NID: g9948977;
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                        PIDN: AAG06280.1;
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K.; Lim,
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C; Superfamily:
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A; Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; A; Title: Deciphering the biology of Mycobacterium A; Reference number: A70500; MUID:98295987 A; Accession: A70597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:Z95120; A;Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N. Rajandream, M. A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, Nature 393, 537-544, 1998
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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ADGIASNTLWPRTMVATAAVQNLLGGDEAMARSRKPEVYADAAYVIVNKPATEYTGKTLL
                                        GE-IAVNALWPKTAIHTAAM-DMLGGPGIESQCRKVDIIADAAYSIFQKPKS-FTGNFVI 244
                                                                                        GTYAVSQACIPHMKGRENPHILTLSPPILLEKKWLRP-TAYMMAKYGMTLCALGIAEEMR
                                                                                                                                 GTYLASKACIPYLKKSKVAHILNISPPLNLNPVWFKQHCAYTIAKYGMSMYVLGMAEEFK 187
                                                                                                                                                                                   ALPIVGDIRDPDAVASAVATTVEQFGGIDICVNNASAINLGSITEVPMKRFDLMNGIQVR
                                                                                                                                                                                                         ALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTR 127
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H37Rv
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Pred. No. 1.3e-41;
7; Mismatches 78
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Pred. No. 8.5e-45;
"" matches 77;
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3 oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) [imported] -
C:Species: Agrobacterium tumefaciens
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-
C:Accession: T44932
R:Kim, K.S.; Farrand, S.K.
J. Bacteriol. 178, 3275-3284, 1996
       J. Bacteriol. 178, 3275-3284
A;Title: Ti plasmid-encoded
by the plant tumor.
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A; Accession: T16638
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                                                                                                                                                                                                                                                                                        MSMTTDDFVKMFSGKLKPTMAFMSGKLKIKGNMALAIKLEKLMNQ 413
                                                                                                                                                                                                                                                                                                                               MADGVKADPTAVKTLKSIVLYIIT -- DGKNELGKFTLDFKSASPSVYLGDVKNGEKANAT
                                                                                                                                                                                                                                                                                                                                                                 VKDSLSDD--VVKATQAIYLFELSGEDG----GTWFLDLKSKGGNVGYGE--PSDQADVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IEAVGGKALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLAGCTVFITGASRGIGKAIALKAAKDGANIVIAAKTAQPHPKLLGTIYTAA-----EE
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                                                                                                                                                                                                                                                  VTVADSDFVDIAAGKLNAQKAFMSGKLKVKGNVMLLQKLQTVLEK 430
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number: Z22872; MUID:96236046
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25.8%;
                                   genes responsible
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Pred. No. 1.8e-13;
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A; Residues: 62-238 <A; Residues: 62-238 <A; Cross-references: 1
C; Genetics: A; Gene: yoxD
C; Superfamily: ribito
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A; Accession: D69930
A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                 Nucleic Acids Res. 15, 8501-8504, 1707
A;Title: Sequence features of the replication terminus of
A;Reference number: S01270; MUID:88040469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) yoxD - B: C;Species: Bacillus subtilis C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000 C;Accession: D69930; S01270
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C;Keywords: oxidoreductase
                                                                                                                                                                                                                                      A;Cross references: GB:Z99114; GB:AL009126; NID:g2634230; A;Experimental source: strain 168 R;Carrigan, C.M.; Haarsma, J.A.; Smith, M.T.; Wake, R.G. Nucleic Acids Res. 15, 8501-8509, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter
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A; Gene: mocc
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A; Status: preliminary;
A; Molecule type: DNA
A; Residues: 1-248 <KIM>
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C; Superfamily: ribitol dehydrogenase;
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                                                                                                                                A; Molecule type:
                                                                                                                                                               A; Accession: S01270
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                                                                               <CAR>
: EMBL:X06168;
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                                                                                  NID: 940205;
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Pred. No. 2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Entian, K.D.; Errington, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                  PIDN:CAA29533.1;
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                                                                                                                                                                                                                                                                                                                           PIDN:CAB13743.1;
                                                                               PID: 9809662
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Carter, N.M.;
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ribitol dehydrogenase;

short-chain alcohol

dehydrogenase homology

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R:anonymous, Genoscope
submitted to the EMBL Data Library, July
A;Description: Pyrococcus abyssi genome
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A;Residues: 1-240 <KAM>
A;Residues: 1-240 <KAM>
A;Cross-references: GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB50558.1; PID:g545907
A;Experimental source: strain Orsay
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A; Accession: H75014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: H75014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Pyrococcus abyssi;Date: 20-Aug-1999;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase
219
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                                                                                                          184
                                                                                                                                               116 LKGAFIVTQEVLRYMKKGKIVNIASIAGKDGGTVGP
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                                                                                                                                                                                                                         56
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                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AADVKDADQVNQAVAQVKEQLGDIDILINNAGISKFGGFLDLSADEWENIIQVNLMGVYH
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                                                                                                                                                                                                                                              KALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLT-NTLDTPTKRLDLMMNVN 125
                                                                                                                                                                                                                                                                                                                    LAGCTVFITGASRGIGKAIALKAAKDGANIVIAAKTAQPHPKLLGTIYTAAEEI-EAVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLLENDHITGE-VIDVN 234
                                                                                                                                                                                  TRGTYLASKACIPYLKKSKVAHILNIS--PPLNLNPVWFKQHCAYTIAKYGMSMYVLGMA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -KGETAVNALWPKTAIHTAAMDMLGGPGIESQCRKVDIIADAAYSIFQKPKSFTGNFVID
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                                                                   RHLAPNILVNAVAP----GPVDTDMLSSE-MKEMLKKLSLTGDIA-----KPSEVAHAVI 218
                                                                                                        EEFKGEIAVNALWPKTAIHTAAMDMLGGPGIESQCRKVDIIADAAYSIFQKPKS-----
                                                                                                                                                                                                                       ETLLVKADVSNREEVREMVKKVIDKFGRIDILINNAGILGKTKDPLEVTDEEWDRVISVN
                                                                                                                                                                                                                                                                                              LKGKVALITGASRGIGRAIAIELAKRGVNVVINYRSNEEEAK-----KTEELCRQYGV
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                                --FTGNFVIDEN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      short-chain alcohol dehydrogenase homology <SADH>
                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        11.4%;
29.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 256; DB 1; L
Pred. No. 1.2e-11;
"""" tches 97;
                                                                                                                                                                                                                                                                                                                                                                                      Score 244; DB 2;
Pred. No. 9.4e-11;
                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       July
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sequence: insights
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                                                                                                                                               --HYAASKGGLIALTFNLA
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glucose 1-dehydrogenase homolog ycdF - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: G69755
C;Accession: G69755
R;Kunst, F: Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C;Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
R;Kunst, F: Ogasawara, N.; Moszer, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
Inch, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari,
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
Iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
y, M.; Ogawa, K.; Ogivara, A.; Oudega, B.; Park, S.H.; Parro, V.; Uphil, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
A;Authors: Schleich, S.; Schroetter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winfers, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A;Accession: G69755
B. Cstraced and Complete School of the Gram-positive bacterium Bacillus subtili
A;Accession: G69755
B. Cstraced and Complete School of the Gram-positive bacterium Bacillus subtili
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G69755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Ric
A;Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: TM1724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRL-----DLM 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGMTKTWAKELAGRNIRVNAVAPGFIETPMTEKLPEKARETALSRIPLGRFGKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INVNLKGVFNVTQMVVPYMIKQRNGSIVNVSSVVGIYGNP----GQTNYAASKAG----V
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69; Conserv
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29.5%;
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Pred. No. 1.6e-10;
l; Mismatches 76;
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dehydrogenase
     not shown;
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homology <SAD>
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A;Cross-references: GDB:385059
C;A;Map position: 5q2-5q2
C;Superfamily: short-chain alcohol dehydrogenase homology
C;Keywords: oxidoreductase
F;10-195/Domain: short-chain alcohol dehydrogenase homology <SAD1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Homo sapi
C; Date: 15-Feb-1996
C; Accession: S59136
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Biochem. J. 311, 437-443, 1995
A;Title: Molecular cloning of a novel widely expressed human 80 kDa 17beta-hydroxystero:
A;Reference number: S59136; MUID:96033037
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F;8-190/Domain: short-chain alcohol dehydrogenase homology <SADH>
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A;Gene: GDB:HSD17B4
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S59136
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A; Residues: 1-736 < ADA>
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                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 134
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Best Local S
  116
                                   118 LDLMMNVNTRGTYLASKACIPYLKKSKVAHILNISPPLNLNPVWFKQHCAYTIAKYGM-- 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 AAAAAWLVSEEASYVTG 241
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nes 74; Conserva
                                                                                60 -EEIRRRGGKAVANYDSVEEGEKV---VKTALDAFGRIDVVVNNAGILRDRSFARISDED 115
                                                                                                                      58 AEEIEAVGGKALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKR 117
                                                                                                                                                                                                                                                         Local Similarity
nes 134; Conserv
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                                                                                                                                                                                            7 RLAGCTVFITGASRGIGKAIALKAAKDGANIVI------AAKTAQPHPKLLGTIYTA 57
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WDIIHRVHLRGSFQVTRAAWEHMKKQKYGRIIMTSSASGIYGNFGQAN--YSAAKLGLLG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSMYVLGMAEEF -- KGEIAVNALWPKTAIHTAAMDMLGGPGIESQCRKV------DI
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                                                                                                                                                                      RFDGRVVLVTGAGAGLGRAYALAFAERGALVVVNDLGGDFKGVGKGSLAADKVV------
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                                                                                                                                                                                                                                                         ; 08
                                                                                                                                                                                                                                                      Score 236; DB 2;
Pred. No. 1.7e-09;
0; Mismatches 175;
                                                                                                                                                                                                                                                                                                 Length 736;
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                                                                                                                                                                                                                                                         Indels 352;
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Qy	176	SMYVLG	Õ
Db	174	: :	w
Оу	191	AVNALWPK 198	œ
뮹	234	GGLFEVGAGWIGKLRWERTLGAIVRQKNHPMTPEAVKANWKKICDFENASKPQSIQESTG 293	ū
Qy	199	204	4
Db	294	: : SIIEVLSKIDSEGGVSANHTSRATSTATSGFAGAIGQKLPPFSYAYTELEAIMYALGVGA 353	ω
Qy	205	AMDMLGGPGIESQCRKV 221	ï
Вb	354	SIKDPKDLKFIYEGSSDFSCLPTFGVIIGQKSMMGGGLAEIPGLSINFAKVLHGEQYLEL 413	ω
Qy	222	DIIADA	
DЪ	414	YKPLPRAGKLKCEAVVADVLDKGSGVVIIMDVYSYSEKELICHNQFSLFLVGSGGFGGKR 473	ω
Qy	235	PKSFTGNFVIDENILKE 251	Ĺ
Db	474	TSDKVKVAVAIPNRPPDAVLTDTTSLNQAALYRLSGDWNPLHIDPNFASLAGFDKPIL 531	μ
Qy	252	EGIENFDVYAIKPGHPLQPDFFLDEYPEAVSKKVE 286	6
В	532	HGLCTFGFSARRVLQQFADNDVSRFKAIKARFAKPVYPGQTLQTEMWKEGNRIHFQTKVQ 591	ī
Qy	287	STGAVPEFKEEKLQLQPKPRSGAVEETFRIVKDSLSDDVVKATQAI 332	2
Db	592	ETGDI-VISNAYVDLAPTSGTSAKTPSEGGKLQSTFVFEEIGRRLKD-IGPEVVKKVNAV 649	9
VQ	333	YLFELSGEDGGTWFLDLKSKGGNVGYGEPSDQADVVMSMTTDDFVKMFSGKLKPTMAF 390	ō
Db	650	FEWHITKGGNIGAKWTIDLKSGSGKYYQGPAKGAADTTIILSDEDFMEVVLGKLDPQKAF 709	ō
Qy	391	MSGKLKIKGNMALAIKLEKLM 411	
DЪ	710	FSGRLKARGNIMLSQKLQMIL 730	
RESULT C83961	12	2	

55 EAIAIQADVADSESVQAMVKETIDTFGAVDILVNNAGITRDNLFMRMKEEDWDAV 109	Db 55 E
67 KALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLM 121	Qy 67 к
2 LOGKTAIVTGASRGIGRATAMELARHGANVVVNYAGNKEKAEKVVAEIKELGV 54	Db 2 L
8 LAGCTVETTGASRGIGKAIALKAAKDGANIVI-AAKTAQPHPKLLGTIYTAAEEIEAVGG 66	0у 8 г
Query Match 11.0%; Score 235; DB 2; Length 246; Best Local Similarity 24.8%; Pred. No. 4.5e-10; Matches 83; Conservative 45; Mismatches 103; Indels 104; Gaps 10;	Query Mat Best Loca Matches
e: fabG	A;Gene: fabG
A;Experimental source: strain C-125 C:Genetics:	A; Experimen
A;Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06210.1; GSPDB:G	A; Cross-ref
A;Molecule type: DNA	A; Molecule
A;Status: preliminary	A;Status: p
A; Accession: C83961	A; Accession
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a A;Reference number: A83650; MUID:20263314	A;Title: Co A;Reference
Nucleic Acids Res. 28, 4317-4331, 2000	Nucleic Aci
R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H	R;Takami, H
C;Accession: C83961	C; Accession
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000	C;Date: 01-
<pre>3-oxoacy1-(acy1-carrier protein) reductase fabG [imported] - Bacillus halodurans (str C;Species: Bacillus halodurans</pre>	<pre>3-oxoacy1-(C;Species:</pre>

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hypothetical protein Rv1928c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-200(
C;Accession: D70635
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris,
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-266 <STO>
A; Cross-references: GB:AE004831; GB:AE004091; NID:g9950347;
A; Cross-references: Strain PAO1
                                                                                                                                                                 RESULT
D70635
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Titte: Complete genome sequence of Pseudomonas aeruginosa PA01, an opp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable short-chain dehydrogenase PA4148 [imported] - Pseudomonas aeruginosa
C;Speciles: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83127
                    Rajandream, M.A.; Rogers, Nature 393, 537-544, 1998
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   A; Authors:
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Best Local S
Matches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase
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                                                                                                                                                                                                                                         173
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                                                                                                                                                                                                                                                                                                                                                                                                              VGGKALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMN 123
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   Sulston,
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   J.E.;
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Pred. No. 5e-10;
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Taylor,
                                                                                                         17-Jul-1998 #text_change 20-Jun-2000
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Whitehead,
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                                                   Hamlin, N.;
 Barrell,
                                     Squares,
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A;Gene: Rv1928c
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase
F;12-194/Domain: short-chain alcohol dehydrogenase homology <SADH>
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A; Residues: 1-255 <COL>
A; Cross references: GB: 284498;
A; Experimental source: strain F
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A;Gencme: plasmid pNGR234a
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F;7-190/Domain: short-chain alcohol dehydrogenase homology <SAD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Freiberg, C.; Fellay, R.; Bairoch, A.; Broug
Nature 387, 394-401, 1997
A;Title: Molecular basis of symblosis between
A;Reference number: 214734; MUID:97305956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 C;Accession: T10877
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C; Species: Rhizobium sp.
A; Variety: strain NGR234
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A; Residues: 1-278 <FRE>
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A;Status: preliminary; nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: translated
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                                TKRLDLMMNVNTRGTYLASKACIPYLKKSKVAHILNISPPLNLNPVWFKQHCAYTIAKYG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAVWDQTMATNLRGTLLCCRQAIPRMIARGGGAIVNMSSCQGLS-
                                                                     -- IAAEAGNALAMAMDIADAQAVAALFETAERHFGGVDLLVNNASAMHLTPRDRAILDLD
                                                                                                        EEIEAVGGKALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLT----NTLDTP 114
                                                                                                                                            RFEGKVAVVTGAGAGIGKACALAIAREGGRVVVADLDGSAAIACTAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 32.
55; Conservative
                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                    34;
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Pred. No. 6.1e-10;
Pred. No. 6.79;
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                                                                                                                                                                                                                Score 232; DB 2;
Pred. No. 8.8e-10;
4; Mismatches 107
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Q9x248 thermotogy

P80869 bacillus :

P51659 homo sapii

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Q01373 neurosporr

P37440 escherichi

Q45219 bradyrhizz

Q08632 picea abia
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MEDLINE-99287316; PubMed-10360571;

A Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

A Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

A McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

A McDonald L., Utterback T.R., Phillips C.A., Richardson D.,

A Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., White O.,

A Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

A Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

Tevidence for lateral gene transfer between Archaea and Bacteria from

Teyidence for lateral gene transfer between Archaea and Bacteria from

Teyidence sequence of Thermotoga maritima.";

L Nature 399:323-329(1999).

C -I- CATALYTIC ACTIVITY: (3R)-3-HYDROXYACYL-[ACYL-CARRIER PROTEIN] +

NADDP(+) = 3-OXOACYL-[ACYL-CARRIER PROTEIN] + NADDPH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVFITGASRGIGKAIALKAAKDGANIVIAAKTAQPHPKLLGTIYTAAEEIEAVGGKALPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKHNIRVSALTPS----TVASDM----SIELN-----LTD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -KGEIAVNALWPKTAIHTAAMDMLGGPGIESQCRKVDIIADAAYSIFQKPKSFTGNFVID 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTRAVLPEMIERKAGDIINISSTAG-----QRGAAVTSAYSASKFAVLGLTESLMQEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TALITGGGRGIGRATALALAKEGVNIGLIGRTS-----ANVEKVAEEVKALGVKAAFA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTRGTYL 131
                                                                                                                                       the Swiss Institute of Bioinformatics and the EMBL outstation opean Bioinformatics Institute. There are no restrictions on its non-profit institutions as long as its content is in no way dand this statement is not removed. Usage by and for commercial is requires a license agreement (See http://www.isb-sib.ch/announce/lan email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39,39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermotoga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 256; DB 1;
Pred. No. 1.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.1.1.100) (3-KETOACYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 238;
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И.,
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Best Local S
Matches 69
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PRINTS; P
PRINTS; P
Fatty aci
NP_BIND
ACT_SITE
SEQUENCE
                                                                                                                                          "First steps from a two-dimensional protein regulation map for Bacillus subtilis."; Electrophoresis 18:1451-1463(1997).
-i- CATALYTIC ACTIVITY: BETA-D-GLUCOSE + NAD(P)H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLUCOSE 1-DEHYDROGENASE_II (EC 1.1.1.47) (GLCDH-II)
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we
                                                                                 -i- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-i- INDUCTION: BY HEAT SHOCK, SALT STRESS,
LIMITATION AND OXYGEN LIMITATION.
-i- SIMILARITY: BELONGS TO THE SHORT-CHAIN
                                                                                                                                                                                                                                                                                                          Submitted (SEP-1997) to
                                                                                                                                                                                                                                                                                                                       Kumano M., Tamakoshi A., Yamane K.;

"A 32 kb nucleotide sequence from the region of the line
resistance gene (22-25 degree) of the Bacillus subtilis
identification of the site of the lin-2 mutation.";
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRESS PROTEIN 74) (GSP74).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DHG2_BACSU
P80869;
                                                                                                                                                                                                                                  Antelmann H.,
                                                                                                                                                                                                                                                  MEDLINE-97443988;
                                                                                                                                                                                                                                                                 STRAIN-
                                                                                                                                                                                                                                                                              SEQUENCE OF 1-13.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus/Staphylococcus
                                                                                                                                                                                                                       Hecker M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110
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                                                                       (SDR) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNVNTRGTYLASKACIPYLKKSKVAHILNISPPLNL~-NPVWFKQHCAYTIAKYGMSMYV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRL-----DLM 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLAGCTVFITGASRGIGKAIALKAAKDGANIVIAAKTAQPHPKLLGTIYTAAEEIEAVGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGMTKTWAKELAGRNIRVNAVAPGFIETPMTEKLPEKARETALSRIPLGRFGKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGMAEEFKGEIA-----VNALWP-------KTAIHTAAMDMLGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RLEGKVCLITGAASGIGKATTLLFAQEGATVIAGDISKE-----NLDSLVKEAEGLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INVNLKGVFNVTQMVVPYMIKQRNGSIVNVSSVVGIYGNP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVDPYVLNVTDRDQIKEVVEKVVQKYGRIDVLVNNAGI-----TRDALLVRMKEEDWDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid biosynthesis; Oxidoreductase; NADP.

ND 10 34 NADP (BY SIMILARITY).

ITE 154 154 BY SIMILARITY.
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PR00081; GDHRDH.
PR01167; INSADHFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                     Bernhardt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                  PubMed=9298659;
nhardt J., Schmid R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26401 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.3%;
29.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus/Clostridium us group; Bacillus.
                                                                                                                                                                                                                                                                                                            the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
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Pred. No. 1.9e-10;
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; 8C08904D28099142 CRC64;
                                                                                      SHORT-CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258
                                                                                                                                                                                                                                   Mach
                                                                                                                                                             NAD(P)(+) -
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                                                                                      DEHYDROGENASES/REDUCTASES
                                                                                                                   OXIDATIVE
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                                                                                                                                                                                                                                                                                                            databases
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                                                                                                                                                                                                                                                                                                                                                     lincomycin-
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                                                                                                                                                               D-GLUCONO-DELTA
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                                                                                                                                                                                                                                     .
П.
                                                                                                                                                                                                                                                                                                                                       chromosome
                              a collaboration -
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
                                                                                                                                                                                                        response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212
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RESULT 4
DHB4_HUMAN
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Best Local S
Matches 74
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Pfam; PF00678; adh_short_C2;
PRINTS; PR00080; SDRFAMILY.
PRINTS; PR00081; GDHRDH.
PROSITE; PS00061; ADH_SHORT;
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entities
or send a
Leenders
de Launoi
                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
ESTRADIOL 17 BETA-DEHYDROGENASE 4 (EC
(17-BETA-HYDROXYSTEROID DEHYDROGENASE
HSD17B4 OR EDH17B4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NP_BIND
ACT_SITE
                                                                        Adamski J., Normand T., Leenders F., Monte Stehelin D., Jungblut P.W., de Launoit Y.; "Molecular cloning of a novel widely expres hydroxysteroid dehydrogenase IV."; Biochem. J. 311:437-443(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase; NADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB000617; BAA22244.1; EMBL; Z99105; CAB12077.1; -. Subtilist; BG12761; ycdf. Interpro; IPR002198; -.
                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                DHB4_HUMAN
P51659;
                              SEQUENCE FROM N.A. MEDLINE-99099251;
                                                                                                                                                        MEDLINE=96033037; PubMed=7487879;
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                          rissue=Liver;
                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225
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 enders F., Do Launoit Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAAAWLVSEEASYVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IADAAYSIFQKPKSFTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVNVTGTFLGAKAALNHMMKNNIKGNVLNISSVHQQIPRPVNVQ-----YSTSKGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTGKTAIVTGSSKGIGKAIAERFGKEKMNVVV-----NYHSDPSGADET-LEIIKQNGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAGCTVFITGASRGIGKAIALKAAKDGANIVIAAKTAQPHPKLLGTIYTAAEEIEAVGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDL-----MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVSVEADVSKEEGIQALLDTALEHFGTLDVMVNNSG----FNGVEAMPHEMSLEDWQRVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
 9251; PubMed=9880674;
Dolez V., Begue A.,
,, Adamski J.;
                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 N
159 B
27776 MW;
                                                                                                                                                                                                                                      Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.1%;
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Pred. No. 4e-10;
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                                                                                                                                                                                                                                      Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Y SIMILARITY.
77842DC45D496C26 CRC64;
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                Moller
                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                           expressed
                                                                                                                                                                                                                                                                                                                                                                                              736 AA
                                                                                                                                                                                                                                                                                                                update)
1.1.1.62) (17-BETA-HSD
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                                                                                                                                         D.,
                Gloeckner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87;
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-!- CATALYTIC ACTIVITY: ESTRAD
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SIMILARITY: BELONGS
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AF057735; AAD08652.1
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Pred. No. 1.9e-09;
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                                 This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-97305956; PubMed-9163424;
MEDLINE-97305956; PubMed-9163424;
MEDLINE-97305956; PubMed-9163424;
                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
PUTATIVE SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE
                                                                                                                                                            "Molecular basis of symbiosis between Nature 387:394-401(1997).
-!- SIMILARITY: BELONGS TO THE SHORT-
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Bacteria; Proteobacteria; alpha
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AE000082; AAB91754.1; P29132; 1DFI.
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                                                                                                                                                            THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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                                                                                                                                                                                       Rhizobium
                                                                                                                                                                                                                Broughton
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FOX2_NEUCR
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Best Local Similarity
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ACT_SITE
SEQUENCE
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Pfam; PF00678; adh_short_C2; 1.
PRINTS; PR00080; SDRFAMILY.
PRINTS; PR00081; GDHRDH.
PROSITE; PS00061; ADH_SHORT; 1.
PROSITE; PS00061; ADH_SHORT; 1.
                                                                                                                                                                MEDLINE-95231521; PubMed-7715608; Fossa A., Beyer A., Pfitzner E., "Molecular cloning, sequencing an
                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF STRAIN-74-OR8-1A / DSM 1258;
                                                                                                                                                     of Neurospora crassa encoding the multifunctional beta-oxidation
                                                                                                                                                                                                                                       NCBI_TaxID=5141;
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                                                                              Gen. Genet. 247:95-104(1995).
FUNCTION: SECOND TRITUNCTIONAL ENZYME ACTING ON THE BETA-OXI
PATHWAY FOR FATTY ACIDS, POSSESSING HYDRATASE-DEHYDROGENASE-
EPIMERASE ACTIVITIES. CONVERTS TRANS-2-ENOYL-COA VIA D-3-
HYDROXYACYL-COA TO 3-KETOACYL-COA.
                                 PATHWAY: BETA-OXIDATION PATHWAY. SUBUNIT: MONOMER (BY SIMILARITY). SUBCELLULAR LOCATION: CATALASE-FREE DOMAIN: CONTAINS TWO SDR DOMAINS.
                       SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVDIIADAAYSIFQKPKSFTGNFV-IDENIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLAGCTVFITGASRGIGKAIALKAAKDGANIVIA-----AKTAQPHPKLLGTIYTAA 58
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278 AA;
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                       TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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BY SIMILARITY.
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                                                                                                                                                                  ., Wenzel B., Kunau W. and sequence analysis
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                                               MICROBODIES
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UCPA_ECOLI STANDARD; PRT; 2
P37440; P77442; P76963; P77140;
01-OCT-1994 (Rel. 30, Created)
01-NOV-1997 (Rel. 35, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
OXIDOREDUCTASE UCPA (EC 1.-.-).
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ACT_SITE
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InterPro; IPR002339; -.
Pfam; PF00175; MacC_dehydratas;
Pfam; PF00106; adh_short; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                           VVKAAIDAF
                                                                                                                                                    VMSMTTDDFVKMFSGKLKPTMAFMSGKLKIKGNMALAIKLEKLMNQMNARL
                                                                                                                                                                              SV---
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Pred. No. 5.6e
54; Mismatches
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BY SIMILARITY.
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BY SIMILARITY.
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  Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuł Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H. Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasun Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K. Yamagata S., Horiuchi T.;
"Construction of a ~~~"."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science [2]
                                                                                                                        use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sirko A., Weglenska A., Hryniewicz M.M., Hulanicka D.M.; "Characterization of the Escherichia coli gene encoding of the short-chain dehydrogenase/reductase (SDR) family. Acta Biochim. Pol. 44:153-157(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAINE-912 / MG1655;
MEDLINE-91426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.
Riley M., Collado-Vides J., Glasner J.,
Gregor J., Davis N.W., Kirkpatrick H.A.,
Mau B., Shao Y.;
                                                                                                                                                                            the
                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                           Borodovsky M., Rudd K.E., Koonin E.N
"Intrinsic and extrinsic approaches
                                                                                                                                                                                                                                                                                                                                        identification of a gene encoding thiosulfate binding.";
J. Bacteriol. 172:3358-3366(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-K12
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Escherichia
                                                                                                                                                                                        between
                                                                                                                                                                                                                                                      Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                        MEDLINE-95075659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Construction of a contiguous 874-kb sequence -K12 genome corresponding to 50.0-68.8 min on analysis of its sequence features."; DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia
                          EcoGene;
                                                                                                                                                                                                                                                                bacterial genome.";
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90264335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97385354; PubMed-9241368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence Science 277:1453-1474(1997).
             InterPro;
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90264335; PubMed=2188959; Hryniewicz M.M., Sirko A., Palucha Sulfate transport
                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restric
                                    L; AE000330; AAC75479.1; D90872; BAA16309.1; D90871; BAA16300.1; CAA68181.1; ALT; M92101; NOT_ANNOTATE

); M32101; NOT_ANNOTATE

); P14061; 1FDV.
                                                                                                                                                                                                                                          SIMILARITY: BELONGS
                                                                                                                                                                                                                            (SDR) FAMILY
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  IPR002198;
IPR002347;
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                                               A68181.1; ALT_INIT NOT_ANNOTATED_CDS
                          ucpA
                                                                                                                                                                                                                                                                                                     PubMed=7984428;
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LONGS TO THE SHORT-CHAIN
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                                                                                                                                                                                                                                                                                           E.V.;
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                                                                                                                                                                                                                                                                                                                                                                 A., Boeck A., Hulanicka in Escherichia coli K-1: novel protein involved
                                                                                                                                                                                                                                                                               for
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                                                                                                                                                                                                                                                                             detecting
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                                                                                                                                                             as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SDR) family.";
                                                                                                                                     . Usage by and for http://www.isb-sib.
                                                                                                                                                                                                                                          DEHYDROGENASES/REDUCTASES
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Mitsuhashi N.,
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Mayhew G.F.,
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Best Local S
Matches 59
                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q45219;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase.
                                                                                                                                                                               Tully R.E., van Berkum P., Lovins K.W., Kelster D.L.;
"Identification and sequencing of a cytochrome P450 gene cluster fro
Bradyrhizobium japonicum.";
Biochim. Blophys. Acta 1398:243-255(1998).
-i- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PROBABLE SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE
Bradyrhizobium japonicum.
Bacteria; Proteobacteria; alpha subdivision; Rhizo
           EMBL; U12678; HSSP; P08074;
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-USDA 110;
                                                                                                                                                                                                                                                                                                                          "Cloning and mutagenesis Bradyrhizobium japonicum symbiotically.";
                                                                                                                                                                                                                                                                                                                                                                      STRAIN-USDA 110;
Tully R.E., Keister D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                           Bradyrhizobium group; Bradyrhizobium NCBI_TaxID=375;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00080; SDRFAMILY. PRINTS; PR00081; GDHRDH.
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                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                               Environ.
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59; Conservative
                                                                                                                                                                     FAMILY.
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                          AAC28892.1; -.
                                                                                                                                                                                                                                                                                                              Microbiol. 59:4136-4142(1993).
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.8e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDR1_PICAB STANDARD: PRT; 271 AA. Q08632; Q1-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation.update) SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE (EC
  Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94120027; PubMed-8290650;
MEDLINE-9411000 H., Pfeiffer F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Picea ables (Norway spruce) (Picea excelsa).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Coniferopsida; Coniferales; Pinaceae; Picea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0080; SDRFAMILY.

PROSITE; PS00061; ADH_SHORT; 1.

Hypothetical protein; Oxidoreductase.

Hypothetical protein; Oxidoreductase.

NP_BIND 10 34 NAD OR NADP (BY SIMILARITY).

ACT_SITE 159 BY SIMILARITY.

SEQUENCE 275 AA; 28827 MW; 312E7070C404DF86 CRC64;
                                                                           PRINTS; PR00080; SDRFAMILY. PRINTS; PR00081; GDHRDH.
                                                                                                                       Pfam; PF00106; adh_short; Pfam; PF00678; adh_short_C
                                                                                                                                                                                                                          EMBL; X74115; CAA52213.1;
HSSP; Q12634; 1YBV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Physiol. 103:1479-1480(1993).
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Isolation and characterization of a cDNA closhort-chain alcohol dehydrogenase from Norway
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                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                               entities requires a license agreement
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Pred. No. 4
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RESULT 10
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01-DEC-1992
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                           Cuphea lanceolata.

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sl

Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

Myrtales; Lythraceae; Cuphea.

NCBI_TaxID-3930;
                                             EMBL; X64566; CAA4581
PIR; S19832; S19832.
HSSP; Q12634; 1YBV.
                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                ELJ
SEQUENCE FROM N.A.
MEDLINE-92293104; PubMed=1376402;
Pawlowski K., Hoericke-Grandpierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DCT-1996 (Rel. 34, Last annotation update)
3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE PR
(3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P28643;
InterPro; IPR002198; -.
InterPro; IPR002347; -.
Pfam; PF00106; adh_shor;
Pfam; PF00678; adh_shor;
                                                                                                                                                                                                                                                                                  "Isolation and characterization of a cDNA from Cuphea lanceolata encoding a beta-ketoacyl-ACP reductase.";
Mol. Gen. Genet. 233:122-128(1992).
-1- CATALYTIC ACTIVITY: (3R)-3-HYDROXYACYL-[ACYL-CARRIER PROTEIN]
NADP(+) - 3-OXOACYL-[ACYL-CARRIER PROTEIN] + NADPH.
-1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
                                                                                                                                                                   between
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                                                                                                                                                                                                                                               SUBCELLULAR
                                                                                                                                       SWISS-PROF entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the ED European Bioinformatics Institute. There are no restructure by non-profit institutions as long as its content
                                                                                                                                                                                                          (SDR) FAMILY.
                                                                                                                                                                                                                                     PLASTIDS
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adh_short; 1.
adh_short_C2;
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                                                                                                                               is not removed.
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Pred. No. 4.
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                                                                                                                http://www.isb-sib.ch/announce/
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FABG_BACSU
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ACT_SITE
SEQUENCE
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Transit peptide.
TRANSIT 1 61 CHLOROPLAST
                                                                               Kunst F.,
Submitted
                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
15-DEC-1998 (Rel. 37, Last sequence u)
30-MAY-2000 (Rel. 39, Last annotation
3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE).
                                                                                                                            MEDLINE-96326321; PubMed-8759840;
Morbidoni H.R., de Mendoza D., Cronan J.
"Bacillus subtilis acyl carrier protein
lipid biosynthesis genes.";
J. Bacteriol. 178:4794-4800(1996).
genome.";
Microbiology 144:801-805(1998)
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                    "A 28 kbp segment from
                                        MEDLINE=98195738;
                                                   STRAIN=168;
                                                            SEQUENCE OF
                                                                                                   STRAIN=168;
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                 STRAIN-168;
                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                           NCBI_TaxID=1423;
                                                                                                                                                                                                                    Bacillus/Staphylococcus
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(NOV-1997)
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                                                                                                                                                                                                                                                                                       sequence update)
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Pred. No. 5.7e-09;
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NADP (BY SIMILARITY)
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                            -KTAIHTAAMDMLGGPGIESQCRKVDIIADAAYSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06BAF0522B2B8C87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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REDUCTASE (EC
                     region
                                                                                                                                                                                                                                                                                                                      246
                     of.
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                                                                                                                                                  Jr.;
encoded
                     the
                                                                                                                                                                                                                              group;
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                                                                               A.;
databases
                     Bacillus
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                     subtilis
                                                                                                                                                   cluster
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RESULT 12
Y325_THEMA
ID Y325_THEMA
AC Q9WYG0;
DT 30-MAY-2000 (1)
DT 30-MAY-2000 (1)
DT 30-MAY-2000 (1)
DE HYPOTHETICAL (GN TM0325.
OS Thermotoga mai
OC Bacteria; Thei
OX NCBI_TaxID=23;
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Best Local S
Matches 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
ACT_SITE
CONFLICT
SEQUENCE
                           Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-- CATALYTIC ACTIVITY: (3R)-3-HYDROXYACYL-[ACYL-CARRIER NADP(+) - 3-OXACYL-[ACYL-CARRIER PROTEIN] + MADPH.
-- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0080; SDRFAMILY.

PRINTS; PRO0081; GDHRDH.

PROSITE; PS00061; ADH_SHORT; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fatty acid biosynthesis; Oxidoreductase; NADP.
NP_BIND 9 33 NADP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002198; -...
InterPro; IPR002347; -...
Pfam; PF00106; adh_short; 1.
Pfam; PF00678; adh_short_C2; 1.
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                                                                                                                                                                                   IGLTKSSAKELASRNITVNAIAP
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TAIVTGASRGIGRSIALDLAKSGANVVVNYSGNEAKANE----
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                                                                                                                                                                                                                                                                                      KAIAVKADVSNPEDVQNMIKETLSVFSTIDILVNNAGI----TRDNLIMRMKEDEWDDV
                                                                                                                                                                                                                                                                                                                KALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRL----
                                                                                                                                                                                                                                                                                                                                                                                             63;
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             Thermotogales;
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23
246
                                                  (Rel. 39, Created)
(Rel. 39, Last sequence up)
(Rel. 39, Last annotation)
L OXIDOREDUCTASE TM0325 (EC)
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ξ.
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31.0%;
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             Thermotoga
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Pred.
                                                                                                                                                                                   184
                                                                                                                                                                                                            197
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D -> A (IN REF
                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                      (EC
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No. 7.
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                                                                update)
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ACID BIOSYNTHESIS
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DHG_BACSU STANDARD; PRT; 2
AC P12310; P94430;
DT 01-CCT-1989 (Rel. 12, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence up
DT 30-MAY-2000 (Rel. 39, Last annotation
DE GLUCOSE 1-DEHYDROGENASE (EC 1.1.1.47).
     OS GED DD AC
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Best Local s
Matches 66
  Bacillus s
Bacteria;
                                                              GDH.
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0080; SDRPAMILY.
PRINTS; PRO0081; GDHRDH.
PRINTS; PRO1167; INSADHFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
Hypothetical protein; Oxidoreductase.
Hypothetical protein; Oxidoreductase.
NP_BIND 10 34 NADP (BY ACT_SITE 152 152 BY SIMIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00106; adh_short; 1.
Pfam; PF00678; adh_short_C2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE001714; AAD35412.1; TIGR; TM0325; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.
STRAIN-MSB8 / DSM 3109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCIVDV-RDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 10.2%; 1 Similarity 30.7%; 66; Conservative 38
                          subtilis
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Firmicutes;
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     Bacillus/Clostridium
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BY SIMILARITY.
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Best Local
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EMBL; D50453; BAA09024.1; -.
EMBL; D99106; CAB12201.1; -.
PIR: S36090; S36090.
HSSP; P19992; 2HSD.
SubtiList; BG10545; gdh.
InterPro; IPR002198; -.
InterPro; IPR002347; -.
                                                                                                                                                                                                                                                                                                     NP_BIND
ACT_SITE
CONFLICT
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Microbiology 142:3047-3056(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glucose dehydrogenase gene.";
J. Bacteriol. 166:238-243(1986).
                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00106; adh_short; 1. Pfam; PF00678; adh_short_C2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00061; ADH_SHORT; 1.
Oxidoreductase; NADP; Sporulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-86168021; PubMed=3082854;
Lampel K.A., Uratani B., Chaudhry G.R., Ramaley R.F., Rudikoff S.
"Characterization of the developmentally regulated Bacillus subti-
glucose dehydrogenase gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus/Staphylococcus group; Bacillus WCBI_TaxID=1423;
170
                           180
                                                      112
                                                                              121
                                                                                                          52
                                                                                                                                    61
                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                            SUBUNIT: HOMOTETRAMER.
INDUCTION: IT IS INDUCED AT STAGE III OF THE SPORULATION.
SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY:
LACTONE + NAD(P)H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SDR) FAMILY.
                        LGMAEEF -- KGEIAVNALWPKTAIHT 203
                                                                              MMNVNTRGTYLASKACIPYLKKSKV-AHILNISPPLNLNPVWFKQHCAYTIAKYGMSMYV
                                                                                                                       MYPD---LKGKVVAITGAASGLGKAMAIRFGKEQAKVVINYYSNKQDPN-----EVKEE
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ETLALEYAPKG-IRVNNIGP-GAINT
                                                                                                        VIKAGGEAVVVQGDVTKEEDVKNIVQTAIKEFGTLDIMINNAGLENPVPSHEMPLKDWDK
                                                    VIGTNLTGAFLGSREAIKYFVENDIKGNVINMSSVHEVIPWPLFVH--YAASKGGIKLMT
                                                                                                                                                                                                                                                                                                     158
148
                                                                                                                                                                                                                     Conservative
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158
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                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                    Score 217; DB 1;
Pred. No. 1.1e-08;
2; Mismatches 83
                                                                                                                                                                                                                                                                                     BY SIMILARITY.
EVI -> AF (IN REF. 1).
; 5894C17DB8F14965 CRC64;
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 193
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                                                                                                                                                                                                                     83;
                                                                                                                                                                                                                                            Length 261;
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RESULT 14
BUDC_KETE
BUDC_KETE
ID COUNTY
OF 01-0CT
DT 01-0CT
CO RIEBSI
RN [1]
RN [1]
RN SEQUEN
RX MEDLIN
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RESULT 15
FOX2_YEAST
ID FOX2_YEAST
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Matches 68
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ACT_SITE
SEQUENCE
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STRAIN-WTT-E-74023;

MEDLINE-93186707; PubMed-8444801;

Blomqvist K., Nikkola M., Lehtovaara P., Suihko M.-L.,

Blomqvist K., Nikkola M., Knowles J.K.C., Penttilae M.E.;

"Characterization of the genes of the 2,3-butanediol operons
Klebsiella terrigena and Enterobacter aerogenes.";

J. Bacteriol. 175:1392-1404(1993).

J. Bacteriol. ACTIVITY: ACETOIN + NAD(+) = DIACETYL + NADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1993 (Rel.
01-OCT-1993 (Rel.
15-DEC-1998 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0080; SDRFAMILY PROSITE; PS00061; ADH_SHOR Oxidoreductase; NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L04507; AAA25056.1; PIR; E47069; E47069.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klebsiella terrigena
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European Bioinformatics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITGASRGIGKAIALKAAKDGANIVIAAKTAQPHPKLLGTIYTAAEEIEAVGGKALPCIVD 74
                                                                                                                                                                                                                               QAAVEAFKKEGHGGKIVNACSQAGHVGN--PEL-
                                                                                                                                                                                                                                                                                                                                                       VRDEQQISAAVEKAIKKEGGIDILVNNASAISLINTLDIPIKRL-DLMMNVNTRGTYLAS
                                                                                                                             TQTAARDLAPLGITVNGFCPGIVKTPMWAE----
                                                                                                                                                                           AEEFKGEIA----VNALWP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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152
241 AA;
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     STANDARD;
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27, Last sequence update)
37, Last annotation update)
REDUCTASE (EC 1.1.1.5) (ACETOIN DEHYDROGENASE) (AR).
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BY SIMILARITY.
     PRT;
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71;
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Pred. No. 1.5e-07,

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01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCT
BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE
(EC 4.2.1.-); D-3-HYDROXYACYL COA DEHYDROGENASE (EC 1.1.1.-)].
FOX2 OR YKR009C OR YK108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92202210; PubMed-1551874;
Hiltunen J.K., Wenzel B., Beyer A., Erdmann R., Fossa A., Kunau W.H.;
"Peroxisomal multifunctional beta-oxidation protein of Saccharomyces cerevisiae. Molecular analysis of the fox2 gene and gene product.";
J. Biol. Chem. 267:6646-6653(1992).
-I- FUNCTION: SECOND TRIFUNCTIONAL ENZYME ACTING ON THE BETA-OXIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duesterhoeft A., Philippsen P.;
"DNA sequencing and analysis of a
centromere CENII of Saccharomyces
unknown open reading frames.";
yeast 8:749-759(1992).
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ACT_SITE
NP_BIND
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SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M86456; AAA34779.1;
EMBL; X65124; CAA46243.1;
EMBL; Z28234; CAA82079.1;
PIR; S25322; S25322.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Saccharomycetales;
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Pfam; PF00106; adh_short; 2.
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PROSITE; PS00342; MICROBODIES_CTER; 1.
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SGD; S0001717; FOX2.
SEQUENCE
                                                                                                                                                                                          DOMAIN
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SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: PEROXISOMAL.
DOMAIN: CONTAINS TWO SDR DOMAINS.
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SHORT-CHAIN DEHYDROGENASE LIKE.
MICROBODY TARGETING SIGNAL (POTENTIAL)
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BY SIMILARITY.
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  66FFD0D49C673788 CRC64;
                         ) (BY SIMILARITY).
SIMILARITY.
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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                          13 VFITGASRGIGKAIALKAAKDGANIVIAAKTAQPHPKLLGTI-----YTAAEEIE
                               IYLFELSGEDGG-----TWFL-----
                                                           YQLSDYNDLIT----
                                                                                        FFLDEYPEAVSKKVESTGAVPEFKEEKLQLQPKPRSGAVEETFRIVKDSLSDDVVKATQA 331
                                                                                                                       KVSNSIFELAAGFFGQLRWERSSGQIFNPDPKTYTPEAILNKWKEITDYRDKPFNKTQHP
                                                                                                                                                   ----SIFQKPKSFTGN-----FVIDENILKEEGIEN----FDVYAIKPGHPLQPD
                                                                                                                                                                                    GLAETLAKEGAKYNINVNSIAP--LARSRMTENVLPPHILKQLGPEKIVPLVLYLTHEST
                                                                                                                                                                                                                 GMAEEF----KGEIAVNALWPKTAIHTAAMDMLGGPGIESQCRKVDIIADAAY-----
                                                                                                                                                                                                                                                DVHLTGGYKLSRAAWPYMRSQKFGRIINTASPAGLFGN---FGQ-ANYSAAKMGL----V 173
                                                                                                                                                                                                                                                                                NVNTRGTYLASKACIPYLKKSKVAHILNISPPLNL--NPVWFKQHCAYTIAKYGMSMYVL
                                                                                                                                                                                                                                                                                                               KAGGIAVANYDSVNENGE--KIIETAIKEFGRVDVLINNAGILRDVSFAKMTEREFASVV 121
                                                                                                                                                                                                                                                                                                                                            AVGGKALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMM 122
                                                                                                                                                                                                                                                                                                                                                                           VYITGAGGGLGKVYALAYASRGAKVVV-----NDLGGTLGGSGHNSKAADLVVDEIK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
-GAGGGLGKSHAIWFARYGAKVVVNDIKDPFSVVEEINKLYGEGTAIPDSHDVV
                                                           ----KAKKL---PPNEQGSVK----IK-SLCNKVVVVT--
                                                                                                                                                                                                                                                                                                                                                                                                                                          50;
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                               -DLKSKGG----NVGYGEPS---DQADVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                             114;
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 381
                               368
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Search completed: June 11, Job time: 137 sec 2001, 16:25:47

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Result
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
244
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2139
1 MLPNTGRLAGCTVFITGASR.....GNMALAIKLEKLMNQMNARL 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         390729 seqs, 57163235 residues
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                                                                                                    Y56815
W16329
R61477
R77866
Y54422
Y96271
                                      Y54424
Y30338
R89323
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                                                                                                    Bacillus D-arabini
Human host cell pr
Clavulanic acid de
S. clavuligerus OR
Amino acid sequenc
B. subtilis glucos
                                                                                                                                                                                                                                                        Description
                    Rape leaf beta-ket
Rape seed beta-ket
                                                            Amino acid sequenc 
A multifunctional
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	G47575	21	285		181.5	5
Arabidopsis thalia	G12202	21	285		81.	44
Aromatic dihydrodi	R66734	16	276		183	43
Glucose dehydrogen	P80063	9	261		8	42
Burkholderia sp. C	B29473	21	277			41
NAD affinity gluco	R27756	13	261		186	40
Sequence of glucos	P80590	9	261		8	39
3-hydroxybutyric a	R94617	17	260			38
Human SCAD family	0	21	292			37
H. ghilianii/B. me	B10741	21	340		œ	36
	B10740	21	272		8	3 5
	0	21	243	٠	9	34
S. pneumoniae fatt	W80670	19	243	٠	189.5	ω ω
 pneumonia 	W38474	19	186	٠	9.	32
Arabidopsis thalia	G12861	21	307		190	31
	G12862	21	285		190	30
	G24786	21	316		190.5	29
	G24787	21	298		190.5	28
Arabidopsis thalia	G50311	21	315		:-	27
	G50312	21	298		:-	26
A. parasiticus ver	Y08329	20	262		•	25
Staphylococcus aur	B15707	21	246		191.5	24
Arabidopsis thalia	G40332	21	307		•	23
Arabidopsis thalia	G40333	21	285		•	22
Thermostable gluco	R24018	13	261		•	21
Glucose dehydrogen	R04044	11	261		•	20
7-alpha-hydroxy st	R22993	13	255		9	19
Mutant yeast multi	Y28712	20	906		197.5	18
ifunct	Y28702	20	906		•	17
Detargeted yeast m	Y28713	20	903	•		16
	Y55986	21	251	•	9	15
Q.	384	11	261	•	198.5	14
Glucose dehydrogen	UT.	13	261	9.3		13
Human short-chain	Y27004	20	313		202.5	12

ALIGNMENTS

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RESULT
Y56815
                Claim 1; Page 10-11; 14pp; Japanese.
                                                                                                                                                                                                                  D-arabinitol dehydrogenase; clinical diagnosis; mycosis.
                                                                                                                                                                                                                                                       31-MAR-2000
                                  Arabinitol dehydrogenase gene encoding D-arabinitol dehydrogenase useful as a clinical diagnosing agent for mycosis
                                                             WPI; 2000-091353/08.
N-PSDB; Z46762, Z46763.
                                                                                                                                                          07-DEC-1999
                                                                                                                                                                            JP11332569-A
                                                                                                                                                                                              Bacillus sp
                                                                                                                                                                                                                                    Bacillus D-arabinitol dehydrogenase
                                                                                                                                                                                                                                                                         Y56815;
                                                                                       (IKED-) IKEDA SHOKKEN KK. (NIPK ) NIPPON KAYAKU KK.
                                                                                                                     26-MAY-1998;
                                                                                                                                      26-MAY-1998;
                                                                                                                                                                                                                                                                                            Y56815 standard; Protein; 258 AA
                                                                                                                                                                                                                                                      (first entry)
                                                                                                                     98JP-0143637
                                                                                                                                       98JP-0143637
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The invention relates to gene encoding D-arabinitol dehydrogenase,

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Best Local (
                                                                                            New isolated DNA which encodes viral interacting proteins - use assays to isolate products for inhibiting viral protein binding which is required for infection, replication, assembly or relea
Non-structural protein 1 interactor 1 (NSII-1) (W16329) is a human host cell protein which interacts with influenza virus protein NSI. It was identified using a yeast interactive trap system. Its amino acid sequence was deduced from NDII-1 cDNA (T63340). Another
                                                                                                                                                                                                                                                                                                                                                                                      NS11-1; non-structural protein 1 interactor 1; host cell protein; influenza virus; replication; antiviral; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W16329;
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                                                                    Disclosure; Fig
                                                                                                                                                                                                                      (MOUN ) MOUNT SINAI MEDICAL CENT
                                                                                                                                                                                                                                                 06-OCT-1995;
                                                                                                                                                                                                                                                                            06-OCT-1995;
                                                                                                                                                                                                                                                                                                       10-APR-1997.
                                                                                                                                                                                                                                                                                                                                 W09712967-A1
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                            Human host cell protein NS1I-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              olated from Bacillus sp. IKD-5A868 strain. The protein can be expressed standard recombinant methodologies. D-arabinitol dehydrogenase is used a clinical diagnosing agent for mycosis. The present sequence presents the D-arabinitol dehydrogenase enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                  1997-226211/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sdassfatggvftidggyti 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAYSIFQKPKSFT--GNFVI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sewaphgvrvntiapgymktkltepyfaaggemidkwlamtpmgrpgvphelggiavyla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGGKALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLAGCTVFITGASRGIGKAIALKAAKDGANIVIA---AKTAQPHPKLLGTIYTAAEEIEA
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70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
76; Conserv
                                                                                                                                                      T63340.
                                                                                                                                                                                             Palese P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                           95WO-US13044
                                                                                                                                                                                                                                                 95WO-US13044.
                                                                    12A-C; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                    replication;
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Pred. No. 1.7e-15;
12; Mismatches 110;
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RESULT
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AC R6
XX
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standard;

Protein;

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R61477 stan R61477; 01-OCT-1995

(first entry)

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Matches 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     host cell protein, NPI-1 (W63327), has also been identified. These host cell proteins can be used in assays to identify cpds. that interfere with the specific interaction between the viral and host cell proteins. Such cpds. can be used to treat viral infection.
                                                                                                                           590
                                                                                                                                                                                       531
                                                                                                                                                                                                                                                   472
                                                                                                                                                                                                                                                                                  233
                                                                                                                                                                                                                                                                                                               412
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les 132; Conserv
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| ||:|| :||: |: ||: ::
ffsgrlkargnimlsqklqmil
                              FMSGKLKIKGNMALAIKLEKLM
                                                                             -hglctfgfsarrvlqqfadndvsrfkavkarfakpvypgqtlqtemwkegnrihfqtkv
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                                                            vfewhitkggnigakwtidlksgsgkvyggpakgaadttiilsdedfmevvlgkldpqka
                                                                                                                        qetgdi-visnayvdlaptsgtsaktpseggklqstfvfeeigrrlkd-igpevvkkvna
                                                                                                                                                       ESTGAVPEFKEEKLQLQP-----KPRSGAVEETF----RIVKDSLSDDVVKATQA
                                                                                                                                                                                                                    EEGIENF------DVYAIK------PGHPLQPDFFLDEYPEAVSKKV
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                                411
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antibiotic; beta-lactamase-inhibitor.

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RESULT
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Best Local Similarity 29.5
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A new enzyme is disclosed which has clavulanic acid dehydrogenase activity, the enzyme having an apparent mol. wt. of 28 kD (by SDS PAGE) and incorporating the N-terminal sequence PSALQGKVALITGASSGIGE. The enzyme is derived from the mycelium of a Streptomyces species, especially S. clavuligerus (e.g. ATCC 27064), S. jumojensis (e.g. ATCC 29864) or S. katsurahamanus (e.g. T272). The present sequence represents the enzyme from S. clavuligerus ATCC 27064.

The enzyme is used to catalyse the biosynthesis of clavulanic acid from a precursor clavulanic acid aldehyde. The obtained clavulanic acid is in turn a key ingredient in the antibiotic Augmentin.
13-NOV-1995 (first entry)
                                               R77866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New clavulanic acid dehydrogenase from Streptomyces, and related DNA and vectors - used to produce beta-lactamase inhibiting clavulanic acid from new 3-oxo:ethylidene analogues
                                                                                       R77866 standard;
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Pred. No. 1.3e-13;
0; Mismatches 96;
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Best Local Similarity 29.8
Matches 71; Conservative
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                 Amino acid sequence
                                                              06-APR-2000
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                    of a beta-ketoacyl-ACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.5%; score 224; DB 16; 29.5%; Pred. No. 1.4e-13; tive 40; Mismatches 96;
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21-OCT-1998;
05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid ester. The specification describes a method for producing a (S)-4-halo-3-hydroxybutyric acid ester. The method comprises asymmetrically reducing 4-halo-acetoacetic acid ester or its derivative with beta-ketoacyl-acyl carrier protein reductase constituting Type II fatty acid synthase, or acetoacetyl-CoA reductase constituting the polybeta-hydroxy fatty acid biosynthesis system. The novel method is used to produce optically active 4-haol-3-hydroxybutyric acid ester, with a high purity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a beta-ketoacyl-ACP reductase protein of Bacillus subtilis. The beta-ketoacyl-ACP reductase enzyme constitut a Type II fatty acid synthetase. The enzyme has an extremely high reducing activity and steroselectivity towards 4-chloroacetoacteic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta-ketoacyl-ACP reductase; Type II fatty acid synthetase; steroselectivity; 4-chloroacetoacteic acid ester; (S)-4-halo-3-hydroxybutyric acid ester; 4-halo-acetoacetic acid ester; beta-ketoacyl-acyl carrier protein reductase; acetoacetyl-CoA reductase; polybeta-hydroxy fatty acid biosynthesis; optically active;
              Y96271;
                                          Y96271 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing optically pure (S)-4-halo-3-hydroxybutyric acid ester
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4-haol-3-hydroxybutyric acid ester
                                                                                                                    164
                                                                                                                                                  180 LGMAEEFKGEIA----VNALWP 197
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                                                                                                                                                                                                             122 MNVNTRGTYLASKACIPYLKKSKVAHILNISPPLNL--NPVWFKOHCAYTIAKYGMSMYV 179
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DB; Z45749.
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                                                                                                                                                                                                                                           kaiavkadvsnpedvqnmiketlsvfstidilvnnagi----
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                                                                                                                                                                                                                                                                                                        taivtgasrgigrsialalaksganvvvnysgneakane------vvdeiksmgr 56
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                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 19-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                              248 AA;
                                                                                                                                                                                                                                                                                                                                                                    Conservative
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98JP-0300178.
99JP-0098205.
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                                                                                                                                                                                                                                                                                                                                                                    36;
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Pred. No. 4.8e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similar activities, carbonyl reductase shows a higher enzymatic activity when used with reduced NADH than with beta-nicotinamide adenine dinuclectide phosphate (NADPH), which is expensive and chemically unstable. The reductase has excellent stereoselectivity producing optically active (S)-4-halo-3-hydroxybutyrate ester with high optical purity and in high yield. (S) 4-halo-3-hydroxybutyrate ester is a useful drug intermediate and is also of importance in alcohol production. The present sequence is the glucose dehydrogenase protein of Bacillus subtilis. Glucose dehydrogenase is important in the regeneration of NADPH. The glucose dehydrogenase gene (A38806) was inserted into a plasmid, already carrying the carbonyl reductase gene of Kluyveromyces aesturii resulting in coexpression of the two genes from the same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carbonyl reductase reduces 4-haloacetoacetate ester to produce (S)-4-halo-3-hydroxybutyrate ester, using reduced beta-nicotinamide adenine dinucleotide (NADH) as an electron donor. This enzyme is useful because it has a high reductase activity for 4-chloroacetoacetate ester but does not substantially dehydrogenate any optical isomers of 4-halo-3-hydroxybutyrate ester. In comparison with other enzymes with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carbonyl reductase; (S)-4-halo-3-hydroxybutyrate ester; drug synthesis; reduced nicotinamide adenine dinucleotide; NADH; alcohol production; 4-haloacetoacetate ester; glucose dehydrogenase; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-DEC-1998;
17-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 20; Page 28-29; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-DEC-1999;
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                                                                                                                                   MMNVNTRGTYLASKACIPYLKKSKV-AHILNISPPLNLNPVWFKQHCAYTIAKYGMSMYV 179
                                                                                                                                                                                                                                                                                                                                          mypd----lkgkvvaitgaasglgkamairfgkeqakvvinyysnkqdpn-----evkee
                                                                                                                                                                                                   vikaggeavvvqgdvtkeedvknivqtaikefgtldiminnaglenpvpshemplkdwdk
                                                                                                                                                                                                                                                                   IEAVGGKALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDL 120
                                                            vigtnltgaflgsreaikyfvendikgnvinmssvhevipwplfvh--yaaskggiklmt
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99JP-0171160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.1%; Score 217; DB 21; 31.6%; Pred. No. 7.2e-13; tive 42; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIJ
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                                                                                                                                                                                                                                                                                       The present sequence represents the glucose dehydrogenase protein of Bacillus subtilis. The glucose dehydrogenase gene was cloned, in the course of the invention, to regenerate the reduced nicotinamide adenine dinucleotide phosphate. The specification describes a method for producing a (S)-4-halo-3-hydroxybutyric acid ester. The method comprises asymmetrically reducing 4-halo-acetoacetic acid ester or its derivative with beta-ketoacyl-acyl carrier protein reductase constituting Type II fatty acid synthase, or acetoacetyl-CoA reductase constituting the polybeta-hydroxy fatty acid biosynthesis system. The novel method is used to produce optically active 4-haol-3-hydroxybutyric acid ester, with a high purity.
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21-OCT-1998;
05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glucose dehydrogenase gene; Type II fatty a steroselectivity; 4-chloroacetoacteic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (S)-4-halo-3-hydroxybutyric acid ester; 4-halo-acetoacetic acid ester;
beta-ketoacyl-acyl carrier protein reductase; acetoacetyl-CoA reductase;
polybeta-hydroxy fatty acid biosynthesis; optically active;
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 18; Page 27-28; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing optically pure (S)-4-halo-3-hydroxybutyric acid ester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-APR-2000
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   112
                              121
                                                               52
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                                                                                                                                         1 MLPNTGRLAGCTVFITGASRGIGKAIALKAAKDGANIVIAAKTAQPHPKLLGTIYTAAEE 60
vigtnltgaflgsreaikyfvendikgnvinmssvhevipwplfvh--yaaskggiklmt 169
                              MMNVNTRGTYLASKACIPYLKKSKV-AHILNISPPLNLNPVWFKQHCAYTIAKYGMSMYV
                                                           IEAVGGKALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDL 120
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DB; 245757.
                                                                                                                       mypd----lkgkvvaitgaasglgkamairfgkeqakvvinyysnkqdpn-----evkee
                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                 261 AA;
                                                                                                                                                                                      Conservative
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98JP-0300178.
99JP-0098205.
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31.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Type II fatty acid synthetase;
                                                                                                                                                                                                     Score 217; DB 21; Pred. No. 7.2e-13;
                                                                                                                                                                                     Mismatches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a multifunctional enzyme designated Fox2. Such multifunctional enzymes may be used in the method of the invention. The specification describes a method for manipulating the metabolism of a plant, and comprises expressing a heterologous gene encoding fatty acid oxidation enzymes in the cytosol or plastids other than the peroxisomes, glyoxisomes or mitochondria of the plant. The method may be used to enhance the biological production of polyhydroxyalkanoates or novel oil compositions in a transgenic plant. Plants which may be used to produce these compounds in this way include Brassicas, maize, soybean,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A multifunctional enzyme designated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y30338;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cottonseed, sunflower, palm, coconut, safflower, peanut, mustards, flax tobacco and alfalfa. The method may also be used to prevent or suppress seed production and therefore increase the production of biomass (leaves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 52-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boynton L, Huisman GW, Snell K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               biomass and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modifying fatty acid metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-540850/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (META-) METABOLIX INC.
   123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 etlaleyapkg-irvnnigp-gaint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 LGMAEEF - - KGEIAVNALWPKTAIHT
                                                            64
                                                                                                                     63
                                                                                                                                                                                                                                 13 VFITGASRGIGKATALKAAKDGANIVIAAKTAQPHPKLLGTI------YTAAEEIE
                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     æ
NVNTRGTYLASKACIPYLKKSKVAHILNISPPLNL--NPVWFKQHCAYTIAKYGMSMYVL 180
                                                         kaggiavanydsvnenge--kiletaikefgrvdvlinnagilrdvsfakmterefasvv 121
                                                                                    AVGGKALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMM 122
                                                                                                                                                                        vvitgaggglgkvyalayasrgakvvv-----ndlggtlggsghnskaadlvvdeik 63
                                                                                                                                                                                                                                                                                             109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stalks)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                       900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               producing specific polymers
                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US04999
                                                                                                                                                                                                                                                                                                                        9.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moloney M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  900
                                                                                                                                                                                                                                                                                             50;
                                                                                                                                                                                                                                                                                       Score 211; DB 20;
Pred. No. 1.8e-11;
0; Mismatches 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in plants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203
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                                                                                                                                                                                                                                                                                             147;
                                                                                                                                                                                                                                                                                                                                                Length 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peanut, mustards, flax,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                             114;
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abolism of
g fatty acid
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
storage compounds, e.g. starch, protein or engineered polymers, or production of plants with enhanced oil content. The DNA may also be used as a probe to obtain similar genes from other plants. The transit peptide may be used to direct other proteins to leaf
                                                   encoding the protein may be inserted in a vector or expression cassette in sense or antisense orientation for expression in an oilseed plant, e.g. for production of transgenic rape plants with low or modified oil content, diversion of metabolism to alternative
                                                                                                          The sequence corresponds to a rape leaf beta-ketoreductase encoded by a cDNA insert in plasmid pJRL6.2 in Escherichia coli XL1-Blue. A plastid stroma targeting transit peptide is present. DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rape; leaf; beta-ketoacyl-ACP-ketoreductase; beta-ketoreductase; plasmid pJR16.2; cDNA library; Escherichia coli; vector; plastid; stroma; transit partia.
                                                                                                                                                                   Claim 2;
                                                                                                                                                                                           New isolated rape beta-ketoreductase with lower or higher oil contents or
                                                                                                                                                                                                                                                WPI; 1996-105914/11
                                                                                                                                                                                                                                                                            Chase D,
                                                                                                                                                                                                                                                                                                       (ZENE
                                                                                                                                                                                                                                                                                                                                                             17-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                 WO9602652-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rape leaf beta-ketoacyl-ACP-ketoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R89323;
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                                                                                                                                                                                                                                                                                                                                  20-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transgenic plant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glaetlakegakyninvnsiap--larsrmtenvlpphilkqlgpekivplvlylthest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FFLDEYPEAVSKKVESTGAVPEFKEEKLOLOPKPRSGAVEETFRIVKDSLSDDVVKATOA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                     Q99305
                                                                                                                                                                                                                                                                                                       ZENECA LTD
                                                                                                                                                                  Page 16; 29pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rapeseed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                napus
                                                                                                                                                                                                                                                                            Elborough K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           crop improvement;
oil.
                                                                                                                                                                                                                                                                                                                                                                                                                                         "Transit peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----kakkl---ppneqgsvk----ik-slcnkvvvvt--
                                                                                                                                                                English.
                                                                                                                                                                                                                                                                            Fentem PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             315
                                                                                                                                                                                                                                                                            Slabas AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lipid; metabolic engineering;
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                                                                                                                                                                                           DNA - used to develop plants with altered oil compsn.
                                                                                                                                                                                                                                                                             White
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                plasmid pJRS10.1; cDNA library; embryo; Escherichia coli; plastid; stroma; transit peptide; cassette; antisense; oil transgenic plant; crop improvement; lipid; metabolic engin polymer; rapeseed oil.
                   Claim 1; Page 15;
                                                                                                 Chase D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plastids
                                     New isolated rape beta-ketoreductase with lower or higher oil contents or
                                                                              WPI; 1996-105914/11
                                                                                                                                         20-JUL-1994;
                                                                                                                                                                                 01-FEB-1996.
                                                                                                                                                                                                    WO9602652-A2
                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                            Brassica napus
                                                                                                                                                                                                                                                                                                                       Rape;
                                                                                                                                                                                                                                                                                                                                          Rape seed
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                                                                                                                     (ZENE ) ZENECA
                                                                                                                                                             17-JUL-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 VFITGASRGIGKAIALKAAKDGANIVI----AAKTAQPHPKLLGTIYTAAEEIEAVGGKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPCIVDVRDEQQISAAVEKAIKKEGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTRG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vvvtgasrgigkaialslgkagckvlvnyarsakeae-----evskqieayggga 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            egasrninvnvvcpgfiasdmtaklgedmekkilgtiplgrygqp--edvaglveflals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E----IAVNALWP----
                                                                                                                                                                                                                                                                                                                        seed; beta-ketoacyl-ACP-ketoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69;
                                                                    Q99304
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                                                                                                Elborough
                                                                                                                                                                                                                                                                                                                                          beta-ketoacyl-ACP-ketoreductase.
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                                                                                                                                                             95WO-GB01678
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                                                                                                                                                                                                                       "Transit peptide"
                 English.
                                                                                                  Fentem
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Pred. No. 1e-11;
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    altered o

                                                                                                  AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 17;
                                                                                                                                                                                                                                                                                                                        beta-ketoreductase;
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                                                                                                  White
                                      o develop plants oil compsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                           engineering;
                                                                                                                                                                                                                                                                                                              vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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The sequence corresponds to a rape seed beta-ketoreductase encoded

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by a cDNA insert in plasmid pJRS10.1 in Escherichia coli XL1-Blue. A plastid stroma targeting transit peptide is present. DNA encoding the protein may be inserted in a vector or expression cassette in sense or antisense orientation for expression in an oilseed plant, e.g. for production of transgenic rape plants with low or modified oil content, diversion of metabolism to alternative storage compounds, e.g. starch, protein or engineered polymers, or production of plants with enhanced oil content. The DNA may also be used as a probe to obtain similar genes from other plants. The transit peptide may be used to direct other proteins to seed
                                                                                                                                                                                                   immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hyportension; neurodegenerative disorder; osteoarthritis; graft vs host disease; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                                                                                                                                                                                                                                                                                                                                         Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
               31-MAR-2000; 2000WO-US08621
                                                      05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B42640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B42640 standard; Protein; 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                    thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ORFX ORF2404 polypeptide sequence SEQ ID NO:4808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYLASKACIPYLKKSKVAHILNISPPLNLNPVWFKQHCAYTIAKYGMSMYVLGMAEEFKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vvvtgasrgigkaialslgkagckvlvnyarsakeae-----evskqieayggga 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VFITGASRGIGKAIALKAAKDGANIVI----AAKTAQPHPKLLGTIYTAAEEIEAVGGKA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               paasyitgqaft 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AYSIFQKPKSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vflctqaatkimmkkrkgriiniasvvgl--ignigqanyaaakag----vigfsktaar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         itfggdvskeadveammktaidawgtidvvvnnagitrdtllirmkksqwdevidlnltg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTRG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        egasrninvnvvcpgfiasdmtaklgedmekkilgtiplgrygqp--edvaglveflals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.7%; Score 206.5; DB 27.4%; Pred. No. 1e-11;
                                                                                                                                                                                     damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
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Y27004 standard;

Protein; 313

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vascoropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; cantiviral; antifungal; antirheumatic; antithflammatory; antibacterial. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative cused to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hyperthematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-1999;
02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C74446 to C77606 encode the proteins given in B40237 to B43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shimkets RA, Leach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CURA-) CURAGEN CORP.
                237
                                                                                             177
                                                                                                                                                                                                            122
                                                    229 YSIFQKPK--SFTGNFVIDENILKEEGIENFDVYAIKPGHPLQ
                                                                                                                                                                      120
                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                                       70
                                                                                                                                                                                                                                                                                                                                                                   10 GCTVFITGASRGIGKAIALKAAKDGANIVIAAKTAQPHPKLLGTIYTAAEEIEAVGGKAL 69
                                                                                                                                                                                                                                                                                                                              7
valatdpnilslsgkvlpscdlarryglrdvd---
                                                                                                                             MAEEFKGE-IAVNALWP---KTAI---HTAAMDMLGGPGIE-----SQCRKVDIIADAA 228
                                                                                                                                                                                                        MNVNTRGTYLASKACIPYLKKSKVAHILNISPPLNLNPVWFKQHCAYTIAKYGMSMYVLG
                                                                                                                                                                                                                                                 gqvcvvtgasrgigrgialqlckagatvyitgr----h---ldtlrvvaqeaqslggqcv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-602362/57
                                                                                                                                                                  nnvglrghyfcsvygarlmvpagqglivvisspgslq---ymfnvpygvgkaacdklaad
                                                                                                                                                                                                                                                                                     PCIVDVRDEQQISAAVEKAIK-KFGGIDILVNNASA--ISLTNT-----LDTPTKRLDLM 121
                                                                                           cahelrrhgvscvslwpgivqtellkehmakeevlqdpvlkqfksafssaettelsgkcv
                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 3990; 5507pp; English
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0540763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0127607.
99US-0127636.
99US-0127728.
                                                                                                                                                                                                                                                                                                                                                                                                                           9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                         54;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 203.5; DB 2
Pred. No. 1.9e-11;
4; Mismatches 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                             118;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    frame
                                                                                                                                                                                                                                                                                                                                                                                                           39;
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                   119
                                                                                                                                                                                                            181
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20-SEP-1999

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Best Local
                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          dehydrogenase enzymes catalyse an irreversible reaction between pyruvate and coenzyme A, to form CO2 and the intermediate COA, in mitochondria. Host cells containing vectors comprising the HSCD nucleic acid may be used to produce the HSCD enzyme, according to standard recombinant DNA methodology. The enzyme may then be used as an antigen in the production of antibodies or in assays to identify antagonists of HSCD activity. These antagonists may then be used to treat disorders associated with inappropriate expression, or over activity of HSCD such as immune disorders and cancers (the antagonist interferes with the reaction between pyruvate and coenzyme A). For example, the antagonists may be used to treat leukemia, lymphomas, adenocarcinomas and cancers of the breast, lung, testis, prostate and brain, Addison's disease, acquired mmune deficiency variations and brain, Addison's disease, acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding human short chain dehydrogenase enzymes useful for the diagnosis, prevention and treatment of disorders associated with abnormal expression of the enzyme, such as immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitochondria; immunė disorder; cancer; leukemia; adenocarcinoma; lymphoma; breast; lung; testis; prostate; brain; Addison's disease; acquired immune deficiency syndrome; asthma; anemia; Crohn's disease; Graves disease; AIDS; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 1A-D; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US5928923-A
                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This represents a human short-chain dehydrogenase (HSCD) enzyme. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Short-chain dehydrogenase;
                                                                                                                                                                                                                                                                                                                                                                                                                            breast, lung, testis, prostate and brain, Addison's disease, acquired immune deficiency syndrome (AIDS), asthma, anemia, Crohn's disease and Graves disease. The nucleic acids and antisense sequences can be used
   177
                                      182
                                                                      120
                                                                                                         122
                                                                                                                                            60
                                                                                                                                                                            70
                                                                                                                                                                                                                                                  10
                                                                                                                                                                                                                                 GCTVFITGASRGIGKAIALKAAKDGANIVIAAKTAQPHPKLLGTIYTAAEEIEAVGGKAL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1999-429503/36
cahelrrhgvscvslwpgivqtellkehmakeevlqdpvlkqfksafssaettelsgkcv
                                   MAEEFKGE-IAVNALWP---KTAI---HTAAMDMLGGPGIE-----
                                                                  nnvglrghyfcsvygarlmvpaggglivvisspgslq---ymfnvpygvgkaacdklaad
                                                                                                       MNVNTRGTYLASKACIPYLKKSKVAHILNISPPLNLNPVWFKQHCAYTIAKYGMSMYVLG
                                                                                                                                         pvvcdssqesevrtlfeqvdreqqgrldvlvnnayagvqtilntrnkafwetpasmwddi
                                                                                                                                                                            PCIVDVRDEQQISAAVEKAIK-KFGGIDILVNNASA--ISLTNT-----LDTPTKRLDLM 121
                                                                                                                                                                                                             gqvcvvtgasrgigrgialqlckagatvyitgr----h---ldtlrvvaqeaqslggqcv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       short-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NC,
                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X86772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                            313 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lal
                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0019216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0019216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dehydrogenase (HSCD)
                                                                                                                                                                                                                                                                                                      9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSCD; enzyme; pyruvate;
                                                                                                                                                                                                                                                                                                      Score 202.5; DB 2
Pred. No. 2.4e-11;
                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enzyme
                                                                                                                                                                                                                                                                                                                     DB 20;
                                                                                                                                                                                                                                                                                   119;
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coenzyme A; human;
                                                                                                                                                                                                                                                                                                                     Length
                                   SQCRKVDIIADAA 228
                                                                                                                                                                                                                                                                                                                       313;
                                                                                                                                                                                                                                                                                   39;
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                         119
                                                                                                                                                                                                               59
                                                                      176
                                                                                                     181
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S. 8

LAGCTVFITGASRGIGKAIALKAAKDGANIVIAAKTAQPHPKLLGTIYTAAEEIEAVGGK 67

legkvvvitgsstglgkxmairfatekakvvvnyrskexean---

---svleeikkvgge

58

Query Match Best Local S Matches 58

. Similarity 29.1 58; Conservative

44;

Score 199.5; DB 13 Pred. No. 3.6e-11; 4; Mismatches 84;

Indels

Gaps

6

DB 13;

Length

261; 13;

9.3%;

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                                    The glucose dehygrogenase enzyme is encoded by a recombinant DNA clone from Bacillus megaterium. The sequence may be mutated by site directed mutagenesis to introduce mutations to the protein sequence (see feature table). The DNA may be used to transform E. coli cells, and transformants may be cultured to mass produce GDH.
                   coli cells, and The mutant GDH i tetramer and is
                                                                                                                            Glucose dehydrogenase prepn. using transformed recombinant from Bacillus megaterium - has specified transformations giglucose dehydrogenase-expressing vector, introduced into E.
                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus megaterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glucose dehydrogenase
Sequence
                                                                                               Claim 1; Page 8;
                                                                                                                                                                      WPI; 1992-354684/43
                                                                                                                                                                                       (AMAN ) AMANO
                                                                                                                                                                                                           13-FEB-1991;
                                                                                                                                                                                                                              13-FEB-1991;
                                                                                                                                                                                                                                                  14-SEP-1992.
                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R27757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R27757 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 valatdpnilslsgkvlpscdlarryglrdvd----
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 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombinant;
                                                                                                                                                                                       PHARM
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                   is not influenced sthermostable.
                                                                                                                                                                                                                                                                                                                                                                            /note-
) 253
                                                                                                                                                                                                                              91JP-0106927
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                                                                                                                                                                                                                                                                                                                                        43
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                              12pp; Japanese.
                                                                                                                                                                                                                                                                                      /label- Leu,
                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; 261
                                                                                                                                                                                                                                                                                                                             label-
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Best Local S
Matches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                        The normal Glu-96 residue is replaced by Lys, Gly or Ala,Gln-252 by Leu or Tyr-253 by Cys. Ser-22 residue can also be Ala, Asp-43 can be Glu, Ala-79 can be Ser and Leu-95 can be Met.E. coli containing this sequence will produce a form of GDH with improved heat stability. the enzymes are useful for glucose assay and can be produced at low costs see also Q03772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glucose dehydrogenase; Bacillus megaterium; glucose assay; ss.
                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New DNA encoding modified forms of glucose dehydrogenase from Bacillus megabacterium, having specific amino acid replacements, with higher heat stability.
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                                                                                                                                                                                 LAGCTVFITGASRGIGKAIALKAAKDGANIVIAAKTAQPHPKLLGTIYTAAEEIEAVGGK 67
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                                                                                                   ALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTR 127
                                                                                                                                                      legkvvvitgsstglgksmairfatekakvvvnyrskedean----svleeikkvgge
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                                                                                                                                                                                                                                                                                                                                                                                        261 AA;
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                                                                                                                                                                                                                                                                                                 This sequence represents the claDH protein which is a putative clavulanate-9-aldehyde reductase used in the biosynthetic pathway for clavulanic acid in Streptomyces clavullegerus. The invention relates to methods of improving production of clavulanic acid by Streptomyces by super-expression of claR gene. The claR gene is characterised in that it is localised in the gene group encoding genes for biosynthesis of clavulanic acid.
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 super-expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Improving production of clavulanic acid
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setvrqevtergvrvvviepgttdtelrghithtatkem----yeqrisqirklqaqdi
                            VLGMAEEF-KGEIAVNALWPKTA-----IHTAAMDMLGGPGIE---SQCRKV---DI
                                                                 MMNVNTRGTYLASKACIPYLKKSK--VAHILNISPPLNLNPVWFKQHCAYTIAKYGMSMY 178
                                                                                                      ltaagakvhvleldvadrggvdaavastvealggldilvnnagimllgpvedadttdwtr 114
                                                                                                                                                        mmpsa--lqgkvalitgrelghrrataralapegaavaiaarrve-----klralgde
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                                                   midtnllglmymtraalphllrskgtvvqmssia----grvtvrnaavyqatkfgvnaf 169
                                                                                                                              IEAVGGKALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDL 120
                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                       Page 8-9;
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                                                                                                                                                                                                           Conservative
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transcriptional regulator;
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Database :
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Maximum Match 100%
Listing first 45 summaries
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1: sp_archea:*
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Gapop 10.0 , Gapext 0.5
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                                                                                     sp_organelle:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	u	2	1		Result	
218	218.5	221	224	224.5	227	227	233.5	235	244	245.5	267	286	302.5	351	665	891.5	1034	1179.5	arose.)))	
10.2	10.2	10.3	10.5	10.5	10.6	10.6	10.9	11.0	11.4	11.5	12.5	13.4	14.1	16.4	31.1	41.7	48.3	55.1	Materia	Query	d
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RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou, X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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Best Local S
Matches 238
O09979
O09979
O1-JUN-1998 (TrEMBLrel. 0
O1-JUN-1998 (TrEMBLrel. 0
O1-MAY-2000 (TrEMBLrel. 1
HYPOTHETICAL 105.9 KDA PR
C17G10.8:
Caenorhabditis elegans.
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HSSP; P47227; IBDB
FLYBASE; FBgn0039537; CG5590.
INTERPRO; IPR002198;
INTERPRO; IPR002347;
INTERPRO; IPR003033;
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PFAM; PF02035; SCP2; 1.
PRINTS; PR00081; GDHRDH.
SEQUENCE 412 AA; 44354 MW
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les 238; Conservative
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PROTEIN C17G10.8 IN CHROMOSOME
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Pred. No. 3.9
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Best Local Similarity
Matches 230; Conserv
                  Q18639;
01-NOV-1996
01-JAN-1998
01-OCT-2000
C45B11.3 PRO'
C45B11.3.
Caenorhabditis elegans
Eukaryota; Metazoa; Ner
                                                                          Q18639
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WORMPEP; C17G10.8; CE16861.
INTERPRO; IPR002198; -.
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SEQUENCE 9
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STRAIN-BRISTOL N2;
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                                     (TrEMBLrel.
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Pred. No. 2.4e-64;
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Nematoda;

Chromadorea;

Rhabditida;

Rhabditoidea;

Rhabditidae;

Peloderinae;

Caenorhabditis

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O05842;
O1-JUL-1997 (TrembLrel. 04, Created)
O1-JUL-1997 (TrembLrel. 04, Last sequence update)
O1-JUN-2000 (TrembLrel. 14, Last annotation update)
HYPOTHETICAL 29.8 KDA PROTEIN.
RV3224 OR MTCYOTD11.02C.
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Bonfield J., Burton J., Connell M., Copsey T., Coolson
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton I.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston I
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkee
Parsons J., Percy C., Rifken L., Roopra R., Sulston J.,
Thlerry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of
MEDLINE-98295987; PubMed-9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Chur Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Badcock K., Basham D., Brown D., Chillingworth T.,
                                                                                                                                                   Mycobacterium tuberculosis.
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                                                                 STRAIN-H37RV;
                                                                           SEQUENCE FROM N.A.
                                                                                                       Actinomycetales;
NCBI_TaxID=1773;
                                                                                                                                   Bacteria; Firmicutes; Actinobacteria;
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NCE 293
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185; Conser
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274029; CAA98431.1;
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AA; 31524
                                                                                                                       Corynebacterineae;
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61.7%;
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III, Tekaia F.,
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Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murph
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers
Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Su
Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from
complete genome sequence.";
Nature 393:537-544(1998).
EMBL; Z95120; CAB08313.1; -.
TUBERCULIST; RV3224; -.
                                                                                                                                                                                                                                                           Maeda M., Kuwayama H.;
"Dictyostellum H504-homolog.'
Submitted (APR-2000) to the I
EMBL; AB042104; BAA94961.1;
SEQUENCE 441 AA; 46387 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                      Dictyostelium discoideum (Slime mold).
Eukaryota; Dictyosteliida; Dictyostelium
NCBI_TaxID=44689;
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Hypothetical protein.
SEQUENCE 282 AA; 29814
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"Molecular characterization of GmFOX2, an evolutionarily highly conserved gene from the mycorrhizal fungus Glomus mosseae, down regulated during interaction with rhizobacteria.";
Mol. Plant Microbe Interact. 12:934-942(1999).
EMBL; AJ243538; CAB55552.1; -.
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                                     GKALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVN
                                                                                                  GKVAIVTGAGGGLGRAYALLLGKLGASVVVNDLGVSAHGQ--GATSSAADKVVEEIRQAG
                                                                                                                                           GCTVFITGASRGIGKAIALKAAKDGANIVIAAKTAQPHPKLLGTIYTAA----EEIEAVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGVFEVGAGWVSKVRLQRSAGVYMKDLTPEKIKDNWAQIESFD----NPSYPTSAS----
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                                                                                                                                                                                                                                       146;
                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                       Conservative
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A; 108897 MW; F6A66FA50EE4D51B
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19.88;
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                                                                                                                                                                                                                                                                      Score 302.5;
Pred. No. 7.
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Q21481;
Q1-NOV-1996
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                                                                                                                       Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Momurray A., Mortimore B., O'Callaghan M.,
Description J., Lloyd C., Momurray A., Mortimore B., O'Callaghan M.,
Description J., Boogle C., Momurray A., Mortimore B., O'Callaghan M.,
Description J., Lloyd C., Momurray A., Mortimore B., O'Callaghan M.,
Description J., Lloyd C., Momurray A., Mortimore B., O'Callaghan M.,
Description J., Lloyd C., Momurray A., Mortimore B., O'Callaghan M.,
Description J., Lloyd C., Momurray A., Mortimore B., O'Callaghan M.,
Description J., Lloyd C., Momurray A., Mortimore B., O'Callaghan M.,
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Description J., Momurray A., Mortimore B., O'Callaghan M.,
Descrip
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                                  Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J. Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; M
Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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e; Peloderinae; Caenorhabditis.
   Weinstock L.,
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 15, Last annotation updat
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Wilkinson-Sproat J.,
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      Wohldman P.;
                                        Waterston
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Best Local Similarity
Matches 120; Conserv
                                              01-NOV-1996
01-NOV-1996
01-OCT-2000
MOCC PROTEIN
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Nature 3
Agrobacterium tumefaciens plasmid pTil5955. Bacteria; Proteobacteria;
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INTERPRO; IPR00303; -.
PFAM; PF00106; adh_short; 1.
PFAM; PF02036; SCP2; 1.
PROSITE; PS00061; ADH_SHORT;
Oxidaradioriasc
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                                               PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                IEAVGGKALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDL |:: ||:: || :: || :: || :| ||
                                                                                                                                                                   VTVADSDFVDIAAGKLNAQKAFMSGKLKVKGNVMLLQKLQTVLEK 430
                                                                                                                                                                            MSMTTDDFVKMFSGKLKPTMAFMSGKLKIKGNMALAIKLEKLMNQ:::: ||| : :|| | ||| : :| : :
                                                                                                                                                                                                                MADGVKADPTAVKTLKSIVLYIIT - - DGKNELGKFTLDFKSASPSVYLGDVKNGEKANAT
                                                                                                                                                                                                                                      VKDSLSDD--VVKATQAIYLFELSGEDG----GTWFLDLKSKGGNVGYGE--PSDQADVV 368
                                                                                                                                                                                                                                                                                                            FEAGAGWYGTIQYYKSKGKVISHASADDIAKNWSTITNMNGAEYIGTITEQSARLVSI--
                                                                                                                                                                                                                                                                                                                                                           SLAQEGAKYNILANTLVPTAGSRLTETVMPQNLVDALKPDYVTPLVTYMVHDSFEESGKV
                                                                                                                                                                                                                                                                                                                                                                                                       IFKVHVKGAYAVTKAAWPYMRDQKYGRIVVTSSNAGVHGNFGQAN--YAAAKSALIGLSN 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                    IKSAGGQAVANYDSVEFGDKI----VKTAIDNFGRIDIVINNAGILRDVSFLKMTELDWDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFDGKVAIVTGAGGGLGKTYALELAKRGCKVVVNDLGGDRH----
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                                                                                                                                                                                                                                                                                                                                 -GGPG----IESQCRKVDIIADAAYSIFQKPKSFTGNFVIDENI--LKEEGIENFDVYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of contiguous nucleotide sequence from chromosome III of C. ^{\mathtt{n}}.
 Proteobacteria; alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 AA;
                                                         (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                        PRELIMINARY;
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THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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Pred. No. 3e-12;
3; Mismatches 1
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 subdivision; Rhizobiaceae group;
                                                         annotation
                                                                       sequence
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Best Local :
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                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLING-97388669; PubMed-9245902;

Kobayashi K., Kobayashi H., Ueda M., F

"Expression of 17 beta-hydroxysteroid retinal pigment epithelium.";

Exp. Eye Res. 64:719-726 (1997).
                                                                                                                                                                                                                                        17-BETA TALLAS.

Gallus (Chicken).

Gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute

Eukaryota; Metazoa; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                        042484 PRELIMINARY; PRT; 735 AA. 042484; 01-JAN-1998 (TrEMBLrel. 05, Created) 01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update) 17-BETA-HYDROXYSTEROID DEHYDROGENASE TYPE IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid.
SEQUENCE
INTERPRO: IPR002198; -.
INTERPRO: IPR002539; -.
INTERPRO: IPR003033; -.
PFAM; PF00106; adh_short; 1.
PFAM; PF01575; MaoC_dehydratas;
PFAM; PF02036; SCP2; 1.
                                                                         FAMILY (SDR).
EMBL; U77911; AAC60249.1;
HSSP; Q12634; 1YBV.
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PFAM; PF00106; adh_short; 1.
PRINTS; PR00080; SDRFAMILY.
PRINTS; PR00081; GDHRDH.
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BL; AF242881; AAB07783.1; -.
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                                                                                                                    SIMILARITY: BELONGS TO THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLAGCTVFITGASRGIGKAIALKAAKDGANIVIAAKTAQPHPKLLGTIYTAAEEIEAVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKGTFLCTQAFFQHMCDRRHGHIINVVS--RARKVASAKFGAYAASKFGM----LGFTQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EALALRTDVQHKSEVDALAKAAFERFGAVDILVNNA-GVAIHNTIPNIKEADWDWMMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -EFKG-EIAVNALWPKTAIHTAAMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 267; DB 2; 1; Pred. No. 2.7e-11; 41; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                            188
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                                                                                                                    SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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Oxidoreductase.
SEQUENCE 735 /
                                         Q9UY54 PRELIMINARY; PRT; 240 AA. Q9UY54; Q1-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation updata) 3-OXOACYL-[ACYL-CARRIER-PROTEIN] REDUCTASE.
Pyrococcus abyssi.
Archaea; Euryarchaeota;
                                                                                                                                                                                      705
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                                                                                                                                                                                                     TMAFMSGKLKIKGNMALAIKLEKLM 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SEIRANGGKAVPNYDSVEDGEKL---VKSALEAFGRIDIVINNAGILRDRSFVRISDED
                                                                                                                                                                                      QKAFFSGKLKVKGNIMLSQKLEMIL 729
                                                                                                                                                                                                                                          NAVEQWDIT-KDGKTAVQWTIDLKNGSGSVYQGPARSSADTTFTLSDQDEMDVVQKKTNP
                                                                                                                                                                                                                                                                                                   KETGDLAIAGGYVDIVSALDKPSALEPTAGLQ----SDLVFEEIGRRIKE-VGHELVRKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YKPLPTSGELRSYSTIADLLDKGSGAYLLIDVNTYCGKDLVCYNQFSLFFVGAGGFGGKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLNDALSQIESQGSISMNSTNSRSVVSSAVDTTSLVGRELTTKVYKYTHLEPILYALGVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEEIEAVGGKALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RFDGRVVLVTGAGGGLGRAYALAFAERGASVVVNDLGGDFKGYGKSSSAADKVV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLAGCTVFITGASRGIGKAIALKAAKDGANIVI-----AAKTAQPHPKLLGTIYTA
                                                                                                                                                                                                                                                                       QAIYLFELSGEDGGT----WFLDLKSKGGNVGYGEPSDQADVVMSMTTDDFVKMFSGKLKP
                                                                                                                                                                                                                                                                                                                            ESTGAV------PEFKEEKLQLQPKPRSGAV-EETFRIVKDSLSDDVVKAT
                                                                                                                                                                                                                                                                                                                                                        LCTFGFAA-RNVLKQ--FANNDVTRFKAIKVRFAKPVFPGQTLQTEMWKEGNRIHFQTKV
                                                                                                                                                                                                                                                                                                                                                                                   SFTGNFVIDENILKEEGIENFDVYAIK------PGHPLQPDFFLDEYPEAVSKKV
                                                                                                                                                                                                                                                                                                                                                                                                                TSEKAKVTVNPPKRPPDAILSDVTTSDQAALYRLSGDWNPLHLDPSFAALGGFQKPILHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SQCRKVDIIAD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SMYVLGMA-----EEFKGEI-----AVNALWPK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSNTIAIEGRKYNIHCNTIAPTAGSRLTQTVMPQDLIDAFKPEYVAPLVLWLCHETCMEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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    Thermococcales; Thermococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 245.5; DB Pred. No. 4.7e-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6D24AD4C7CC5179D CRC64;
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                                                         update)
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RESULT 11
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Best Local S
Matches 76
                                       Query Match
Best Local Similarity
Matches 83; Conserv
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                                                                                                                                                                                                                                                                      Q9KA03;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
3-OXOACYL-(ACYL-CARRIER PROTEIN) REDUCTASE (EC 1.1.1.100).
                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-C-125 / JCM 9153;

Takami H., Nakasone K., Takaki Y.;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; APO01515; BAB06210.1; -.
                                                                                                               Oxidoreductase. SEQUENCE 246
                                                                                                                                                                                                                                     Bacillus halodurans.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/StaphyJococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                         Q9KA03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Pyrococcus abyssi genome sequence: insights into archaeal structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ248288; CAB50558.1; -.
HSSP; P50163; 2AE1.
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[1]
                                                                                                                                                                                                                            NCBI_TaxID=86665;
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LAGCTVFITGASRGIGKAIALKAAKDGANIVI-AAKTAQPHPKLLGTIYTAAEEIEAVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKGAFIVTQEVLRYMKKGKIVNIASIAGKDGGTVGP------HYAASKGGLIALTFNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRGTYLASKACIPYLKKSKVAHILNIS--PDLNLNPVWFKQHCAYTIAKYGMSMYVLGMA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAGCTVFITGASRGIGKAIALKAAKDGANIVIAAKTAQPHPKLLGTIYTAAEEI-EAVGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLT-NTLDTPTKRLDLMMNVN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKGKVALITGASRGIGRAIAIELAKRGVNVVINYRSNEEEAK-----KTEELCRQYGV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RHLAPNILVNAVAP----GPVDTDMLSSE-MKEMLKKLSLTGDIA-----KPSEVAHAVI
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                                                                                                                246 AA;
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                26126 MW;
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                                       11.0%; Score 235; DB 2;
24.8%; Pred. No. 4.7e-09;
Live 45; Mismatches 103
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Pred. No. 1
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                                                                                                               852B95EB8DEE9E90 CRC64;
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..le-09;
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                                                                  Length
                                          Indels 104;
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                                                                                                                                                                                                                                RX MEDLINE-98295987; PubMed-9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd S., RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., RA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., RA Taylor K., Whitehead S., Barrell B.G.; T. Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence."; L. Nature 393:537-544(1998).
R MSSP; P50163; 2AE1.
R TUBERTITTEN ENTONOM:
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                                    Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             RV1928C OR MTCY09F9.36.

MYCObacterium tuberculosis.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
                                                                                                                                                                INTERPRO; IPR003015; -.
PFAM; PF00106; adh_short; 1.
PFAM; PF00678; adh_short_C2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 13, Last sequence update)
01-UN-2000 (TrEMBLrel. 14, Last annotation updat
HYPOTHETICAL 27.0 KDA PROTEIN.
                                                                                             Hypothetical protein. SEQUENCE 255 AA; 27031 MW;
                                                                                                                 PROSITE; PS00038; HELIX_LOOP. PROSITE; PS00061; ADH_SHORT;
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinomycetales;
NCBI_TaxID=1773;
                                                                                                                                                                                                    INTERPRO; IPR002198; -. INTERPRO; IPR002347; -.
                                                                                                                                                                                                                            TUBERCULIST; Rv1928c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158
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                                                Local
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               8
                                                            Match
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LAGCTVFITGASRGIGKAIALKAAKDGANIVIAAKTAQPHPKLLGTIYTAAEEIEAVGGK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVIDENILKEEGIENFDVYAIKPGHPLQPDFFLDEYPEAVSKKVESTGAVPE-FKEEKLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNVNTRGTYLASKACIPYLKKSKVAHILNISPPLNLNPVWFKQHCAYTIAKYGMSMYVLG
:: | :| : | : | | | : | : | : | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QIPLARLGQPEEVAKAVRFLASDDASYLTGQTIHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOPKPRSGAVEETFRIVKDSLSDDVVKAT-QAIYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAEEFKGEIAVNALWPKTAIHTAAMDMLGGPGIESQCRKVDIIADAAYSIFQKPKSFTGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGLTKTLARELANRNITVNAVAPG:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDTNLKGVFHCSKAVTRPMMKQRFGRIINVSSVVG------AIGNAGQANYVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAIAIQADVADSESVQAMVKETIDTFGAVDILVNNAGI----TRDNLFMRMKEEDWDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRL-----DLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LQGKTAIVTGASRGIGRATAMELARHGANVVVNYAGNKEKAEKVVA-----EIKELGV
                                     l Similarity
65; Conser
                                                                                                                                            PR00080; SDRFAMILY. PR00081; GDHRDH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                HELIX_LOOP_HELIX; UNKNOWN_1.
                                               10.9%;
                                     29;
                                   Score 233.5; DB 2
Pred. No. 6.4e-09;
9; Mismatches 79
                                                                                                                   UNKNOWN_1.
                                                                                             454692E6FAA253FF
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                                    79;
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                                   Indels
                                                          Length
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                                   29;
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                                   Gaps
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 RESULT
Q9XAB2
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RESULT
Q9K3Y7
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Best Local S
Matches 64
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Bentley S.D.,
Submitted (JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9K3Y7 PRELIMINARY; PRT; 253 AA. Q9K3Y7; Q9K3Y7; Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) PUTATIVE SHORT CHAIN OXIDOREDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                      Redenbach M., Kieser H.M., Denapaite D., Eichner A
Kinashl H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic a
the 8 Mb Streptomyces coelicolor A3(2) chromosome.
Mol. Microbiol. 21:77-96(1996)
EMBL; AL359949; CAB95803.1; -
SEQUENCE 253 AA; 25937 MW; 608F0D5C1AE55A8A CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor. Bacteria; Firmicutes; Ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oliver K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinomycetales; Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2SCG61.28C
175
                                 188
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                                 GETAVNALWP - - - KTAIHTAAMDMLG
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FGVTANAVAPGF IATEMTKATADRVG
                                                                                                     TYLASKACIPYLKKSKVAHILNISPPLNLNPVWFKQHCAYTIAKYGMSMYVLGMAEEF-K 187
                                                                                                                                                                           LPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTRG 128
                                                                                                                                                                                                            VTGAARGIGAATALRLAAEGRAVAVIDLDEAACK------DTVEKITAAGGKA 57
                                                                                                                                                                                                                                               ITGASRGIGKAIALKAAKDGANIVI-----AAKTAQPHPKLLGTIYTAAEEIEAVGGKA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLTKAMAVELAPHKIRVNSVSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTR
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                                                                  AFLMTKACQKHMVDAKFGRVVNLSSSSALGN---RGQVNYSAAKAGLQGFTKTLAKELGK
                                                                                                                                          IAVGCDVSDEAQVEAAVARIAEELGAPTILVNNAGVLRDNLLFKMSVSDWDTVMNVHLRG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVPVCCDVSQHQQVTSMLDQVTAELGGIDIAVCNAGIITVTPMLDMPLEEFQRLQNTNVT 121
                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (JUN-2000)
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                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parkhill
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                                                                                                                                                                                                                                                                                                  10.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barrell B.G., Rajandream
e EMBL/GenBank/DDBJ databa
                                                                                                                                                                                                                                                                                  Score 227; DB
Pred. No. 1.8e
33; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193
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                                                                                                                                                                                                                                                                                                                                                                          608F0D5C1AE55A8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinobacteridae;
                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eichner A.,
                                                                                                                                                                                                                                                                                     83;
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databases
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A.
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RESULT
053398
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AC 01
DT 01
DT 01
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Best Local S
Matches 82
053398;
01-JUN-1998
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9XAB2
Q9XAB2;
01-NOV-1999
01-NOV-1999
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUTATIVE OXIDOREDUCTASE.
SCF43A.03.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO; IPRO02347; -.
PFAM; PF00106; adh_short; 1.
PRINTS; PR00080; SDRFAMILY.
PRINTS; PR00081; GDHADH.
SEQUENCE 679 AA; 71668 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Redenbach M., Kieser H.M., Denapaite D., Eichner A Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic a the 8 Mb Streptomyces coelicolor A3(2) chromosome. Mol. Microbiol. 21:77-96(1996).
EMBL; AL096837; CAB48890.1; -.
HSSP; P25529; IAHH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seeger K., Harris D.;

"A set of ordered cosmids and a detailed genetic and physical the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         James K.D., Parkhill
Submitted (JUL-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPR002198; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97000351; PubMed-8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                      625
                                                                                                                                                                                                                                                         462
                                                                                                                                                                                                                                                                                 62
                                                               15
                                                                                                                                                                                                                                                                                                                                  2 LPNTGRLAGCTVFITGASRGIGKAIALKAAKDGANIVIAAKTAQPHPKLLGTIYTAAEEI 61
                                                                                                    EEKLGEFYAQRTLLKRE---
                                                                                                                            KSFTGNFVIDENILKEEGIENFDVYAIKPGHPLQPDFFL
                                                                                                                                                       QVRLLAAEL-GEHGIRVNGVNPDGVVRGSGI-FAGGWGAKRA-----AVYGV---P
                                                                                                                                                                             YVLGMAEEFKGE--IAVNALWPKTAIHTAAMDMLGGPGIESQCRKVDIIADAAYSIFQKP
                                                                                                                                                                                                                             LMMNVNTRGTYLASKACIPYLKKSKV-AHILNISPPLNLNPVWF-KQHCAYTIAKYGMSM 177
                                                                                                                                                                                                                                                         EELGGDDKAVAVTVDVTSEEQIAAAFQAAALAFGGVDLVVNNAGISISKPLLETSAKDWD
                                                                                                                                                                                                                                                                        EAVGG--KALPCIVDVRDEQQISAAVEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLD 119
                                                                                                                                                                                                                                                                                                          MPRPKPLATRVALVTGAGSGIGKAIARRLVDEGACVVVADLNAE------NAAAVA 461
                                                                                                                                                                                                       LQHDIMARGSFLVSREAARVMTAQELGGDIVYIA---SKNAVFAGPNNIAYSATKADQAH
                                                                                                                                                                                                                                                                                                                                                             82;
                                                                                                                                                                                                                                                                                                                                                                         Similarity
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(TrEMBLrel.)
(TrEMBLrel.)
 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                      PRELIMINARY;
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12,
 96,
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                                                                                                                                                                                                                                                                                                                                                             41;
Created)
Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                    ---VLPEHVANAVFAL
                                                                                                                                                                                                                                                                                                                                                                       Score 227; DB 2;
Pred. No. 8.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                             Mismatches
 sequence update)
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                                                                                                    654
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HSSP; P14061; 1FDU.
TUBERCULIST; RV1050; -.
INTERPRO; IPR002198; -.
PFAM; PF00106; adh_short;
SEQUENCE 301 AA; 3249;
                                                                                                                                                                                                                                                                                                                       MEDLINE-98295987; pubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.,
Taylor K., Whitehead S., Barrell B.G.;
Teciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
BMBL; AL021897; CAA17166.1; -.
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NCBI_TaxID=1773;
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AA; 32497
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113 AW299683

171 BF979524

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AW966207 EST378280
AA315514 EST187305
AW29963 xs42e02.x
BF679524 602288151
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prime, mRNA:

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/clone="CLDB0052B08"
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
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8 LTI_NFL006_PL2 |
mRNA sequence.
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                        Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
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    www.genoscope.cns.fr.

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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, 1
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens Eukaryota; Metrazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metrazoa; Chordata; Catarrhini; Hominidae; 1 (bases 1 to 602)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collect
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               196
                                                                                                                                                                                                                           e: LLAM9755 row: k column: quality sequence stop: 602.
          /db_xref="taxon:9606"
/clone="IMAGE:3921920"
/clone=lib="NIH_MGC_72"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin: Vector: pcwV-SpoRT6; Si Site_2: Sali; Cloned unidirectionally. Pri Average insert size 2 kb. Library constru Technologies."
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Query Match Best Local Similarity

22.8%;

Score :

584;

Length

602;

DB 141; 8.6e-298;

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BF699109
BF699109.1 GI:11984517
                                   CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1115 row: 1 column: 08
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National Institutes of Health, Mammalian
Unpublished (1999)
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602126730F1 NIH_MGC_56
                                                                                                                               Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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/db_xref="taxon:9606"
/clone="IMAGE:4283671"
/clone_lib="NIH_MGC_56"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (TI phage-resistant)"
/lab_host="DH10B (TI phage-resistant)"
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                                                                                                   620 bp mRNA EST 03-NOV-1999 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623752 WP:C17G10.8 CE16861 FAT-3: ALCOHOL DEHYDROGENASE;
                           GI:6199963
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491; Conserva
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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Unpublished (1997)
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Seq primer: -40UP from G1bco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
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Location/Qualifiers
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC/DCTD/DTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 963)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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Mammalia; Eutheria;
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Llarity 100.0%;
Conservative
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/db_xref="taxon:9666"
/db_xref="taxon:9666"
/clone="TMAGE:3919890"
/clone_1lb="NHI_MGC_72"
/tlssue_type="melanotic melanoma"
/tlssue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
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Primates;
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         atactgctgctgaagaaattgaagcagttggaggaaaggccttgccatgtattgttgatg
                                                     caaatattgttattgctgcaaagaccgcccagccacatccaaaacttctaggcacaatct
                                                                                                                              | tcacaggtgcaagccgtggcattggcaaagctattgcattgcattgaaagcagcaaaggatggag
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Assessment of gene expression patterns in a model metastasis using a 19,200 element cDNA microarray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: John Quackenbush
The Institute for Genomic
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
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gde,P., Q1,R., Abernathy,K.,

I.E., Saeed,A.I., Sharov,V.,
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301 838 3528
301 838 0208
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                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGI"
/note="Vector: pBluescriptSKm"
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Pred. No. 1.5e-222;
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2E 1 (bases 1 to 487)

3S Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult (C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White (O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald (Line, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald (Line, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald (Line, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald (Line, T.R., Cotton, M.C., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Shirley, R., Kelley, J.C., Kelley, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weddman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wel, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
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The Institute for Genomic |
9712 Medical Center Drive,
                                                                                                                                                                                                                                 For clone availability, additional sequence and exinformation related to this EST, please check the Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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EST187305 Colon carcinoma
                                                                                                                                                                                                                                                                                                                            Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Kerlavage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Other_ESTs: THC130362
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                                                               /organism="Homo sapiens"
/db_xref="ARCC (inhost):110493"
/db_xref="taxon:9606"
/clone_lib="Colon carcinoma (HCC)
/tissue_type="colon"
                                                                                                                                                                                     Location/Qualifiers
1. .487
/cell_type="KM12C"
/cell_line="KM12C(HCC)-parental human
;Dukes B2"
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Tissue Procurement: Christopher Moskaluk, M.D., P
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CCAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lini.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                     AW299683 692 bp mRNA
xs42e02.x1 NCI_CGAP_Kidl1 Homo
similar to TR:019066 019066 OV
                                                                                                                                                     Unpublished (1997)
Contact: Robert Strausberg,
Tel: (301) 496-1550
                                                                                                                                                                                                    Tumor Gene Index
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                        Robert_Strausberg@nih.gov
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ECORI; Site_2: XhoI"
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                                                                                                                                                                                                                                                                                                                                                                                         gtcagatcaagcagtaaaattagctctttcaaatcttcttgtcatgtaaaatgaagctag
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ccctttgagccttacatctcattcactgtctttctccaagaaaagtattttgggcggaca 2344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAGATAGAATTTGTCTCTAAAAGACTTGAAATTGTAATTAAAATGGCAAGCTAATCAAA
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                                                                                                                                                                                                                                                                                                              TCTGTTTTAAAATTTTTAGTTTTGGATTGTATACTAATGAAAATCTTAATGATGTTTT
                                                                                                                                                                                                                                                                                                                                                                           GTCAGATCAAGCAGTAAAATTAGCTCTTTCAAATCTTCTTGTCATGTAAAATGAAGCTAG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCTTTGAGCCTTACATCTCATTCACTGTCTTTCTCCAAGAAAGTATTTTGGGCGGACA 177
Unpublished (1999)
Contact: Robert Strausberg,
Tel: (301) 496-1550
                                         Eukaryota; Metazoa; Chordata; Craniata; Vu
Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 829)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian (
                                                                                                                                                                                    mRNA sequence.
BF979524
                                                                                                                                                                                                                 BF979524 829 bp
602288151F1 NIH_MGC_97
                                                                                                                                                                       BF979524.1
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llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"

/note="Organ: kidney; Vector: pT773D-Pac (Pharmacia) with
/note="Organ: kidney; Vector: Not I; Site_2: Eco RI;
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
plasmid DNA from the normalized library NCI_CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 132376-132391, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo. "
27 a 130 c 93 g 242 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE: 2772314"
/clone_lib="NCI_CGAP_Kidll"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 418; DB 113;
Pred. No. 7.6e-210;
                                                                                                                                                                                                                     Homo
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                   맑
                                                                                                                                                                                                                     sapiens
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                                                                                                            Vertebrata;
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                                              Gene
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                                              Collection (MGC)
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BASE COUNT
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                                                                                                                                            RESULT 1
AA305116
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                                                           ACCESSION
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Best Local
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                                                                                                                                                                                                                              | CCaaaagccaaaaagttttactggcaactttgtcattgatgaaaatatcttaaaagaaga 1516
                                                                                                                                                                                                                                                                                                                                                                                                                       tggtatcgaaagccagtgtagaaaagttgatatcattgcagatgcagcatattccatttt 1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         caatgcattatggcctaaaacagccatacacactgctgctatggatatgctgggaggacc 1396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtatggtatgtctatgtatgtgcttggaatggcagaagaatttaaaggtgaaattgcagt 1336
                                                                                                                                                                                                                                                                        aggaatagaaaattttgacgtttatgcaattaaaccag 1554
                                                                                                                                                                                                                                                                                                                                                                                                 TGGTATCGAAAGCCAGTGTAGAAAAGTTGATATCATTGCAGATGCAGCATATTCCATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCACCACTGAACCTAAATCCAGTTTGGTTCAAACAGCACTGTGCTTATACCATTGCTAA
                                                                                                                                                                                                                                                                                                                CCAAAAGCCAAAAAGTTTTACTGGCAACTTTGTCATTGATGAAAATATCTTAAAAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAATGCATTATGGCCTAAAACAGCCATACACACTGCTGCTATGGATATGCTGGGAGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTATGGTATGTCTATGTATGTGCTTGGAATGGCAGAAGAATTTAAAGGTGAAATTGCAGT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               AA305116.1
EST.
                                                       AA305116 462 bp mF
EST176117 Colon carcinoma
5' end, mRNA sequence.
AA305116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://image.llnl.gov
Plate: LLAM10036 row: f column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgr); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NHM/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:4373773"
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/db_xref="taxon:9606"
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                                       GI:1957444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.5%; Score 398; DB 171; 100.0%; Pred. No. 3e-199;
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                                                                                                II Homo sapiens cDNA
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181
                                               910
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C.J., Lee, N. H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White
C.J., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,
Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald
L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,
Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.M.,
Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Wediman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W.,
Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,
Kunsch, C., Hungjun, J., Li, H., Meissner, P., Kim, A.K., Kozak, D.L.,
Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P. J., Fannon
,M.R., Rosen, C.A., Haselline, W.A., Fields, C., Fraser, C.M. and
Venter, J.C.
                      ttctaggcacaatctatactgctgctgaagaaattgaagcagttggaggaaaggccttgc
                                                                                                                                                                                                                      gatgtacagtttttatcacaggtgcaagccgtggcattggcaaagctattgcattgaaag 849
TTCTAGGCACAATCTATACTGCTGCTGAAGAAATTGAAGCAGTTGGAGGAAAGGCCTTGC
                                                                                             CAGCAAAGGATGGAGCAAATATTGTTATTGCTGCAAAGACCGCCCAGCCACATCCAAAAC
                                                                                                                         cagcaaaggatggagcaaatattgttattgctgcaaagaccgcccagccacatccaaaac
                                                                                                                                                                                             GATGTACAGTTTTTATCACAGGTGCAAGCCGTGGCATTGGCAAAGCTATTGCATTGAAAG
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443; Conser
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Institute for Genomic Research 9712 Medical Center Drive, Rockvil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    For clone availability, additional sequence and exinformation related to this EST, please check the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Other_ESTs: THC130362
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                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: colon; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
96 c 110 g 111 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="colon"
/cell_type="Caco-2"
/cell_line="Human colon adenocarcinoma;ATCC HTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="ATCC (inhost):128605"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex⇒"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Colon carcinoma (Caco-2) cell line
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99.8%;
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                     Score 393; DB 5; I
Pred. No. 1.3e-196;
0; Mismatches 1;
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The WashU-Merck EST Project
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
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Fax: 314 286 1810
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/db_xref="GDB:1240187"
/db_xref="taxon:9606"
/clone="IMAGE:295266"
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Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
Insert Size: 3243
High quality sequence stops: 326 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 3243 Std Error: 0.00
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Hillier, L., Clark, N.,
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Fax: 314 286 1810
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/db_xref="GDB:413643"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTGTGTTTTTATATTTCAAGGGTTTAACCCTTTGAGCCTTACATCTCATTCACTGTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA622988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA622988 386 bp mRNA EST 21-OCT-1997 np58h04.sl NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130551 similar to WP:C17G10.8 CE02490 ALCOHOL DEHYDROGENASE;, mRNA
                                                                                                                          www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 937 Std Error: 0.00
                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 386)
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                                                                                                                                                            cDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                    National Cancer Institute, Cancer
                                                                                                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                        primer: -40m13 fwd. ET from Amersham
h quality sequence stop: 342.
                                                                                                                                                                                                                                                                                                                (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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a 64 c 89 g 172 t 7 others
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1130551"
                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:2526864
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Pred. No. 4.2e-161;
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Matches 325
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MEDLINE
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219446.1
Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex,
Tel: 33169472800
                                                                                                                                Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.

IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                              Z19446 340 bp mRNA EST 10-FEB-1993
HSB28F112 STRATAGENE Human skeletal muscle cDNA library, cat.
#936215. Homo sapiens cDNA clone 28F11, mRNA sequence.
                                                                                                                       and
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                  Genexpress-Genethon
                                                                                     95277534
                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                 GI:29287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="NCI_CGAP_Br2"
                                                                                                    Sci. III,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.7%; score 325; DB 9; L
100.0%; Pred. No. 1.4e-160;
Live 0; Mismatches 0;
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Search completed: June 12, Job time: 5425 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genexpress@genethon.fr strand(+), single read warning|| There has been some controversy in the scientific literature over
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              possible contamination of this library by yeast and prokaryotic sequences.
See Science 259:1677-1678 (1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.4%; Score 317; DB 159; Length 340; ilarity 100.0%; Pred. No. 2.5e-156; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="skeletal muscle"
/dev_stage="19 years"
/note="Organ: leg muscle; Vector: Lambda ZAPII; Tissue
from female, 19 years old, normal leg muscle. Cloning
from female, 19 years old, normal leg muscle. Cloning
vector is Lambda ZAPII, in vivo excision from lambda ZAPII
to pBluescript SK(+). Genexpress library reference is B. "
47 c 59 g 127 t 1 others
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/db_xref-"GDB:DOS6990E"
/db_xref-"taxon:9606"
/clone-"28F11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                   13:10:48
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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| SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
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Maximum Match 100%
Listing first 45 summaries
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2561
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:/SIDSZ/gcgdata/geneseq/yeneseqn/NA198.DAT: *
:/SIDSZ/gcgdata/geneseq/geneseqn/NA198.DAT: *
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DNA sequence which Sequence complemen Human T lymphotrop HTLV-I LTR genomic HTLV-I long termin HTLV-I p21x cDNA.
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SR alpha enhancer/
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163	163	163.6	163.6	164.6	166	166	166	166	166	166	166	166	166	166	166	166	166	166	166	166	166	166	166	166	166	166	166	166	166	166.2	7.	180.4	181.4
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16	16	20	20	20	18	17	18	19	19	19	17	21	21	19	19	20	18	18	17	μ W	17	21	20	21	19	20	20	20	21	20	19	21	13
Q94114	T51451	X57235	X57224	V86402	T60558	T27558	T60555	V22139	V22129	V22130	T15286	245253	Z45251	V09006	V09005	X33862	T59271	T47202	T27555	Q30906	T27556	239629	X84028	Z45931	V02043	X08456	X08455	X08454	A27831	X84027	V02042	C08959	Q25258
Expression vector	Plasmid pSVI7.ID.L	WO 9923223 Seq ID	WO 9923223 Seq ID	EST clone AR253.	Recombinant trans-	Shuttle vector pAd	pAdCMVgag	sequence of	e f	cDNA sequence of p	Ad.AV.CMVLacZ hybr	Expression vector	Expression vector	Vector containing	Vector containing	AV.CMVLac2 cis pla	•	nant ado	Shuttle vector pAd	Synti	٧e	DNA sequence of pl	MMP9 promoter beta	Nucleotide sequenc	Plasmid pWRG3196 e	AAV vector sequenc		AAV vector sequenc	Vector plasmid pCM	MMP9 promoter GFP		ecreted p	HindIII fragment o

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WPI; 1998-312407/27 P-PSDB; W55047. Key mat_peptide Secreted protein; membrane-associated protein; protein secretion; signal peptide; alkaline phosphatase; ptrAP3; vector; reporter; s: Vector ptrAP3 DNA sequence V27206; (MILL-) MILLENNIUM BIOTHERAPEUTICS INC 06-NOV-1997; 28-MAY-1998. WO9822491-A1 Homo sapiens. 12-OCT-1998 V27206 standard; cDNA; 4951 BP. 19-NOV-1996; DP, (first entry) Levinson 96US-0752307 97WO-US20201 Location/Qualifiers 1313.2782 /*tag- a /product= human placental alkaline phosphatase DA, McCarthy SA; SS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC expression vector contains a cDNA encoding human placental alkaline CC expression vector contains a cDNA encoding human placental alkaline CC phosphatase (AP, see w55047) lacking a slygnal sequence. When CC phrap3 is transfected into a mammalian cell line, such as COS7 CC cells, AP protein is neither expressed nor secreted since the AP CC cDNA of ptrAp3 does not encode a signal peptide or a membrane CC anchor sequence. However, insertion of a cDNA encoding a signal CC peptide sequence into ptrAp3 facilitates the expression and CC secretion of AP upon transfection of the DNA into mammalian cells. CC The presence of AP activity in the supernatants of transfected CC cells therefore indicates the presence of a signal sequence in the CC cDNA of interest. This forms the basis of a novel method for the CC cDNA of interest. This forms the basis of a novel method for the CC consecution of genes encoding novel proteins having a signal CC sequence, i.e. secreted or membrane-associated proteins of CC designated ethb0018f2, was isolated clone (see V27707), CC designated ethb0018f2, was isolated using the novel method and CC encodes a human neural adhesion protein (see W55045) protein having CC antitiple, consecutive IGG domains. The method is very sensitive CC antermation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 656;
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transforming bacteria and
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96.2%;
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Pred. No. 1.8e-78;
0; Mismatches 14;

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                       This DNA sequence comprises the HindIII/XhoI fragment of the CC SR alpha enhancer/promoter in plasmid pobl-SR alpha 296. The SR alpha enhancer/promoter is composed of human T cell leukaemia CC virus 1 5 untranslated sequences and the SV40 enhancer. It is creported to increase expression from the SV40 enhancer/promoter by C10-fold in host cells, and is active in a broad range of cell types. The SR alpha enhancer/promoter has been utilised in CC expression vectors designed for efficient expression of genes in cultured cells. The invention provides vectors and improved methods for the expression and co-amplification of genes encoding recombinant proteins in cultured cells. The methods permit the classification of cell lines which have co-amplified input recombinant sequences which encode an amplifiable marker, one or more expression vectors encoding a protein of interest and optionally a selectable marker. The amplified cells provide large quantities of recombinant proteins suitable for immunotherapy for treatment of custom vaccines, including multivalent vaccines that reflect the constant constant variation found in a patient's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                Multivalent vaccine to treat B cell lymphoma or leukaemia comprises at least 2 different recombinant variable region
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01-MAY-1996;
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Chimeric -
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                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 104; 177pp; English.
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I cell leukaemia
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Sequence 633 BP; 114 A;

210 C;

155 G; 154 T; 0 other,

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Test system for detecting inhibition - using vector
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                                                                                                                                                    cytokine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   487;
                                                                                                                                                  apoptosis; guanine phosphoribosyltransferase; gpt; luciferase;
e; tumour necrosis factor; interleukin-1; inhibitory effect;
                                                                                                                                                                         of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                   CYTOSIGNAL
                                                                                                                                            signal transmission;
                                                                                 97WO-JP04126
                                                                                                                                                                         specification
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96.1%;
intra-cellular signal transmissi containing apoptosis-inhibiting
                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 400; DB 18;
Pred. No. 3.2e-54;
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Chloramphenicol;

acetyltransferase;

vector;

vector

for

increased

17-MAY-1990

entry)

N92604 standard;

DNA;

ВP

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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is used in the plasmid vectors of the invention. The vectors which comprise a gene which can induce apoptosis under specific conditions, e.g. guanine phosphoribosyltransferase (gpt)), or a reporter gene, e.g. luciferase, where the gene is situated downstream of a promoter which responds to specific extracellular stimulation such as the presence of a cytokine, e.g. tumour necrosis factor (TNF) or interleukin-1. The vector may be used to transform a suitable cell line, such as a cell line which does not produce hypoxanthine-guanine phosphoribosyl transferase (HGPRT). The transformed cells are used to test the inhibitory effect of a gene or substance on intracellular signal transmission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reporter gene and promoter sequence, potential anti-inflammatory agents
  591
                                      474
                                                                              531
                                                                                                                  414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 91.3 nes 464; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 aggcagaagtatgcaaagcatgcatctcaaattagtcagcaaaccatagtcccggcccct 60
                                                                                                                                                                                                                                                                                                            cgaggggctcgcatctctccttcacgcgccgccgcctacctgaggccgccatccacgc
                                                                                                                                                                                                                                                                                                                                                                                    ttccagaagtagtgaggaggcttttttggaggcctaggctttttgcaaaaagctcctcgat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aactccgcccatcccgcccctaactccgncccagttccggcccattctccgccccatggc 120
gtttc-gttttctgttctgcgccgttac
                    gtttcagttttctgttctgcgccgttac
                                                                                                taggtaagtttaaagctcaggtcgagaccggggctttgtccgggcgctcccttggagccta
                                                                                                                                                                                                                                                     cggttgagtcgcgttctgccgcctcccgcctgtggtgcctcctgaactgcgtccgccgtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tgactaattttttttttatttatgcaga-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aggcagaagtatgcaaagcatgcatctc-aattagtcagc-aaccatagtccc-gcccct 194
                                                                            taggtaagtttaaagctcaggtcgagaccgggcctttgtccggcgctcccttggagccta
                                                                                                                                                                                                                                 cggttgagtcgcgttctgccgcctcccgcctgtggtgcctcctgaactgcgtccgccgtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aactccgcccatcccgccctaactccgccc--agttccgcccattctccgccccatggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tgactaattttttttatttatgcagaggccgaggccaagcttgcctcggcctctgagcta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 A; 210 C; 156 G; 153 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.8%;
91.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 354.2; |
Pred. No. 4.4e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -gccgaggccgcctcggcctctgagcta 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g. screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Best Local S
Matches 271
      gene expression; regulation;
human T-cell leukaemia; HIV;
                                                                                                                                                                                                                                                                       HTLV-I LTR is inserted into pSV-CAT, the region gives 10-100 fold CAT expression. in a wide range of animal cells for high
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
LTR
 gene
                                                                T42902
                                                                                                                                                                                                                                                                                                            Recombinant DNA vector - contains HTLV-I long terminal repeat ligated part of U5, for increased chloramphenicol acetyltransferase activity.
                                       16-JUN-1997
                                                                                                                                                                                                                                                             Sequence 755
                                                                                                                                                                                                                                                                                                Disclosure; ; ; Japanese.
                                                                                                                                                                                                                                                                                                                                           (GANK ) GAN KENKYUKAI ZH
                                                                                                                                                                                                                                                                                                                                                        28-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                     28-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                                              JP01277489-A
                                                                                                                                                                                                                                                                                                                                                                                                                                          LTR
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mes 271; Conservative
                                                                                                                                                                                                  ggggctcgcatctctccttcacgcgccgccgccctacctgaggccgccatccacgcgg
 therapy;
                                                                                                                                                ttgagtcgcgttctgccgcctcccgcctgtggtgcctcctgaactgcgtccgccgtctag
                                                                                               tc-gttttctgttctgcgccgttacagatcgaa 623
                                                                                                      tcagttttctgttctgcgccgttacagatccaa 509
                                                                                                                       standard; DNA;
                         which regulates
                                                                                                                                                                                                                                                           BP; 161 A; 255 C; 178 G; 161 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                        88JP-0105677
                                                                                                                                                                                                                                                                                                                                                                     88JP-0105677
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/label= R
582..755
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/label= U5
354..581
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/label-
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1..353
                                      entry)
                                                                                                                                                                                                                                   10.1%;
                                                                9045
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                                                                ВP
                                                                                                                                                                                                                             0;
      plasmid; viral infection;
antivirus agent; detectic
                                                                                                                                                                                                                            Score 259.4; DB 1
Pred. No. 2.7e-32;
0; Mismatches 1
                         expression in HTLV and
                                                                                                                                                                                                                                                                       U3 region is lost, and the Vector can be integrated levels of expression.
                                                                                                                                                                                                                                         DB 10; Length
      detection;
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      cancer;
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RESULT
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Query Match
Best Local Similarity 99.3
                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a DNA molecule with gene expression regulation activity. This sequence is used in a plasmid for regulation of gene expression, and treatment of viral infection pref. human T-cell leukaemia and HIV. The plasmid also encodes a protein which is used as an antivirus agent, and also in a method for detecting cancer. The DNA molecule and protein have potential uses in gene therapy, and the plasmid may also have potential use in the treatment of TSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA molecule with gene eve.g. treatment of human vand for detecting cancer
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9045 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-455367/45.
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24-MAR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Igarashi H, Okumura
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                                                                                                                                                                                                                                            ggggctcgcatctccttcacgcgccgccgccctacctgaggccgccatccacgccgg
                 tcagttttctgttctgcgccgttacagatccaa 509
                                                                                                                                        gtaagtttaaagctcaggtcgagaccgggcctttgtccggcgctcccttggagcctacct
                                                                                                                                                                                 ttgagtcgcgttctgccgcctcccgcctgtggtgcctcctgaactgcgtccgccgtctag
                                                             gtaagtttaaagctcaggtcgagaccgggcctttgtccggcgctcccttggagcctacct
tc-gttttctgttctgcgccgttacagatcgaa 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Page 38-43; 77pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95JP-0104299
95JP-0066559
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8584..8589
/*tag b
8278..9032
/*tag c
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1..757
/*tag= a
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99.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression regulation T-cell leukaemia and
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                                                                                                                                                                                                                                                                                                          Score 259.4;
Pred. No. 3.5e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                        DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV, as antivirus a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sakaguchi
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                                                                                                                                                                                                                                                                                                                                        Length 9045;
                                                                                                                                                                                                                                                                                                                                                                                      other;
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1:

N40080 standard; cDNA;

99.38;

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Query Match
                                     Diagnosis of human leukaemia and/or lymphoma and virus infection made with part or all of the recombinant DNA. Virus antigenic proteins can be produced. These peptides and proteins, and antibodies against them, are useful for the diagnosis, therapy ar prevention of human leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
5'UTR
                                                                                                                                                                     (NICA-)
                                                                                                        Viral genomic DNA complementary to RNA of human leukaemia virus useful in recombinant DNA producing therapeutic and diagnostic
                                                                                                                                                                                                                                                                                                                                    CDS
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                       Sequence
                                                                                   Claim 4; Table 1, Page 11-15; 23pp;
                                                                                                  proteins
                                                                                                                                 WPI; 1984-172336/28
                                                                                                                                                                                             07-DEC-1982;
                                                                                                                                                                                                            06-DEC-1983;
                                                                                                                                                                                                                           11-JUL-1984
                                                                                                                                                                                                                                          EP113078-A.
                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                       3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosis; therapy; prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence complementary to the genome of adult T-cell leukaemia virus (ATLV) ATK-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N40080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T-cell leukaemia virus
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                                                                                                                                                                     JAPAN FOUND FOR CAN GAN KENKYUKAI ZH.
                                                                                                                                                               JURIDICAL FOUND
                        9047
                                                                                                                                               Sugano
                        вP;
                                                                                                                                                                                             82JP-0214287.
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/product= env
6834..7130
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9033..9047
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/*tam-
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802..2088
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/product=
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278..9032
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                        2087 A; 3164 C;
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 10.1%;
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 Score 259.4;
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                       1713 G;
                                                                                   English.
                        2083
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                       Τ,
                        0 other;
Length 9047;
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N90825
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Best Local Similarity Matches 271; Conserva
                            Conferring resistance to retro-virus infection upon host cells using polynucleotide which directs transcription of RNA which inhibits replication
                                                                                                                                                                                                                                                                                                                                                                           HTLV-1; HTLV-1; LTR; retrovirus; inhibition; resistance; antisense therapy; anti-R; anti-PBS; primer binding site; anti-S; splice site; anti-TAT; anti-ART; anti-ARG; anti-POL; anti-CAP; anti-AUG; translation initiation site; ss.
        Disclosure; Fig 3; 43pp; English
                                                                        P-PSDB;
                                                                         WPI; 1989-265197/37
P-PSDB; P95426.
                                                                                                          Greatbatch W,
                                                                                                                              (GREA-) GREATBATCH GEN-AID
                                                                                                                                                     16-FEB-1988;
                                                                                                                                                                          16-FEB-1989;
                                                                                                                                                                                                13-SEP-1989.
                                                                                                                                                                                                                      EP331939-A.
                                                                                                                                                                                                                                                                                                                                                      Human T
                                                                                                                                                                                                                                                                                                                                                                                                                                Human T lymphotropic virus 1 long terminal repeat
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22-JAN-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                       lymphotropic virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                                                                          Sanford
                                                                                                                                                     88US-0156188
                                                                                                                                                                          89EP-0102692
                                                                                                                                                                                                                                                                                    /*tag= a
449..720
/*tag= b
                                                                                                                                                                                                                                              /product= GAG_protein_(part)
/note= "Partial open reading frame only; does not include termination codon and initiator Met
                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA;
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                                                                                                                                                                                                                                                                                                                                                     type 1.
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                                                                                                                                                                                                                                           translated product"
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Best Local Similarity
Matches 194; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        To confer retroviral resistance on a cell, the cell is transformed with a vector comprising a polynucleotide coding for RNA which is complementary or homologous to a nucleic acid sequence within at least one gene from the retroviral genome and which inhibits replication of the retrovirus. Particularly preferred target genes are those coding for the ENV, POL, GAG proteins. Antisense sequences may also target the ART and TAT splice sites, the region around the translation initiation codon (AUG) or the primer binding site (PBS) of the retrovirus. The method is especially intended to confer resistance to infection by human immunodeficiency virus (HIV), feline leukeemia virus (FELV) or human T lymphotropic virus i (HTLV-I). This sequence is from the long terminal repeat of HTLV-I and represents a target for inhibitory nucleic acid of the
                                         28-JUN-1994.
                                                                    US5324643-A
                                                                                                                                                  Human lymphotropic virus type
                                                                                                                                                                               AUG
                                                                                                                                                                                       HIV; HTLV-1; FeLV; long terminal repeats; LTR; target fragments; resistance; retroviral infection; infection process; retroviral replication; reverse transcription; translation; complementary; antisense; 3'R-region; primer binding site;
                                                                                                                                                                                                                                                             HTLV-1 LTR genomic fragment.
                                                                                                                                                                                                                                                                                      07-FEB-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                            Q68398 standard; RNA; 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
              16-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention.
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he sequence
                                                                                                                                                                             codon region; RNA splice sites; ss
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              88US-0156188
                                                                                                         Location/Qualifiers 452..720
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Pred. No. 9.7e
70; Mismatches
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Best Local Sim
Matches 194;
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                                 HIV: human immunodeficiency virus; antisense; replication inhibitor; infection resistant; retrovirus; lymphotropic disease; viral leukaemia; lymphadenopathic; HTLV-I; human T-cell lymphotropic virus type I; AIDS;
                       acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conferring resistance to retroviral polynucleotide which is transcribed inhibits infection into host cells.
                                                                                    HTLV-I long terminal repeat region oligonucleotide
                                                                                                              21-MAY-1997
                                                                                                                                                               T47852 standard; RNA; 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      retroviral diseases.
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29-JUL-1991;
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                        immune
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                                                                                                             (first entry)
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91US-0739718
                        deficiency
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                                                                                                                                                               ВP
                       syndrome; PCR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 249.4;
Pred. No. 9.7e
70; Mismatches
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                        polymerase chain
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T-cell lymphotropic

Virus

type

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RESULT 10
Q50836
ID Q50836
XX
AC Q50836
XX
DT 09-MAY
XX
DE HTLV-1
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Best Local
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16-FEB-1988;
29-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             747850-T47852 are long terminal repeat (LTR) region polynucleotides of human immunodeficiency virus (HIV), feline immunodeficiency virus (FIV) and human T-cell lymphotropic virus type I (HTLV-I), respectively. Antisense oligonucleotides against these polynucleotides are used in a method for conferring resistance to retroviral infection on a host cell. The antisense sequences are transfected into the host cell to prevent viral replication by binding to a site important for this process, e.g. the LTR, PBS (primer binding site). R region (essential for the "first transfer the transfer that the t
                                    09-MAY-1994
                                                                                                   Q50836 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the LTR, PBS (primer binding site), R region (essential for the "first jump" of reverse transcription), start codon or certain sites in the 3' and 5' untranslated regions. Resistant cells can be introduced into a patient, e.g. by bone marrow transplant to provide protection against retroviral infection.
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 HTLV-1 p21X cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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88US-0156188.
91US-0739718.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 249.4; DB 18;
Pred. No. 9.7e-31;
70; Mismatches 6;
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RESULT 11
Q50835
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Best Local Similarity
Matches 230; Conserv
                                                                            Homo
                                                                                                                                                                    HTLV-1 tax/rex splice region.
                                                                                                                                                                                                                                                    Q50835;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Q50835) shows cDNA prepared from RNA extracted from a HTLV-1 infected cell. This was amplified by PCR and was used to construct p21x cDNA (Q50835). Primers and probes were then manufactured (Q50837-43), these are useful for the detection of HTLV-1 infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligo-nucleotide primer - for detecting mRNA of human leukemia virus 1 by polymerase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTLV-1; human T cell leukemia virus;
24-SEP-1993.
                                      JP05244999-A
                                                                                                              detection; splice;
                                                                                                                                  HTLV-1; human T
                                                                                                                                                                                                              09-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1675 BP; 349 A; 613 C; 336 G; 377 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                    agacteageeggetetecaegetttgeetgaeeetgettgeteaaeteta 1675
                                                                                                                                                                                                                                                                                                                                                                                                          1993-338952/43
                                                                        sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gtaagtttaaagctcaggtcgagaccgggcctttgtccggcgctcccttggagcctacct 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ttgagtcgcgttctgccgcctcccgcctgtggtgcctcctgaactgcgtccgccgtctag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ttgagtcgcgttctgccgcctcccgcctgtggtgcctcctgaactgcgtccgccgtctag 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.0%; Score 230; DB 14; llarity 100.0%; Pred. No. 1.1e-27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; 19pp; Japanese.
                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91JP-0354839
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                                                                                                                                    cell leukemia
                                                                                                                                                                                                                                                                                        cDNA; 1866
                                                                                                                  SS
                                                                                                                                                                                                          entry)
                                                                                                                                virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR;
                                                                                                                                  PCR;
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                                                                                                                                  polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1675;
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                                                                                                                                    chain
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18-DEC-1991;

91JP-0354839

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RESULT
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ID Q21
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Best Local S
Matches 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Q50835) shows cDNA prepared from RNA extracted from a HTLV-1 infected cell. This was amplified by PCR and was used to construct p21x cDNA (Q50836). Primers and probes were then manufactured (Q50837-43), these are useful for the detection of HTLV-1 infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligo-nucleotide primer - for detecting {\tt mRNA} of human leukemia virus 1 by polymerase chain reaction
                                         WPI;
                                                            Caput D,
                                                                                                                                                                                                                                                 HindIII fragment of pSE1.
                                                                                                                                                                                                                                                                                                              Q25258 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1866 BP; 394 A; 678 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-338952/43.
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and parasitic disease
        New monocyte chemo:attractive cytokine - for treatment and parasitic infections, e.g. leishmaniasis, leprosy
                                                                                (ERAP
                                                                                                                                                                                                                    mouse;
                                                                                                                                                                                                                               Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OIHS)
                                                                                                                29-NOV-1990;
                                                                                                                                   29-NOV-1991;
                                                                                                                                                         03-JUN-1992.
                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                      26-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                    417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.0%;
Local Similarity 100.0%;
nes 230; Conservative (
                                                                                                                                                                                                                                                                                                                                  12
                                                                                                                                                                                                                                                                                                                                                             gtaagtttaaagctcaggtcgagaccggggcctttgtccggcgctcccttggagcctacct
                                         1992-185765/23
                                                                                                                                                                                                                                                                                                                                                                                                                                               ttgagtcgcgttctgccgcctcccgcctgtggtgcctcctgaactgcgtccgccgtctag
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ttgagtcgcgttctgccgcctcccgcctgtggtgcctcctgaacttgcgtccgccgtctag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) SHIONOGI &
                                                                                                                                                                                                                   ne; plasmid pSE1; HTLV-1; human T-lymphocyte virus;
alpha-globin; E.coli cloning vector; ds.
                                                                                ELF SANOFI.
SANOFI SA.
                                                            Ferrara P,
                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91JP-0354839
                                                                                                                90FR-0014961
                                                                                                                                    91EP-0403243
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                                                                                                                                                                                                                                                                                                              422 BP
                                                            Miloux B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 230; DB 14;
Pred. No. 1.1e-27;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 386 G; 408 T; 0 other;
                                                            Minty A,
                                                             Vita
                   treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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          or Chagas
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This fragment contains a sequence close to the 5'-UTR of HTLV-1 and the mouse alpha-globin distal intron. The fragment is used in the construction of plasmid pSE1 which was designed as a cloning vector in E.coli and an expression vector in animal cells
                                   New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond diagnostic, forensic, gene therapy and chromosome
                  Claim 1; SEQ
                                                                                                                                                                                                                                                  Human; 5' EST;
                                                                                                                                                                                                                                                                     Human secreted
                                                                                                                                                                                                                                                                                           06-OCT-2000
                                                                                                                                                                                                                                                                                                              C08959;
                                                                                                                                                                                                                                                                                                                                 C08959 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1b; 45pp;
                                                                                                  Dumas
                                                                                                                                         26-FEB-1999;
                                                                                                                                                           21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                06-SEP-2000
                                                                                                                                                                                                   EP1033401-A2
                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                         gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ggctcgcatctctccttcacgcgccgccctacctgaggccgccatccacgccggtt 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                              aggctccaag--ggagccggacaaaggcccggtctcgacctgagctctaaacttacctag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gagtcgcgttctgccgcctcccgcctgtggtgcctcctgaactgcgtccgccgtctaggt 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gagtegegttetgeegeeteeegeetgtggtgeeteetgaactgegteegeegtetaggt 358
                                                                              2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                 -gttttctgttctgcgccgttacaacttcaaggtatg
                                                                                                 Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q25259-Q25262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP;
                   ID 13034;
                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                          chromosome mapping;
                                                                                                                                                                                                                                          expressed sequence tag; chromosome mapping; ss.
                                                                                                                                         99US-0122487
                                                                                                                                                                                                                                                                       protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66
                                                                                                                                                                                                                                                                                                                                 CDNA;
                                                                                                                                                                                                                                                                                         entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 C; 121 G; 93
                 71pp + CD-ROM;
                                                                                                  Duclert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   French
                                                                                                                                                                                                                                                                       EST,
                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 181.4; D
Pred. No. 3.7e-
                                                                                                                                                                                                                                                                       SEQ ID NO: 13034
                                                                                                 P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                  Giordano
                  English
                                                                                                                                                                                                                                                   secreted protein; cDNA isolation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0 other;
                                                                                                                                                                                                                                                                                                                                                                                   277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36; Indels
                                   tag (5' EST) for
to 5'ESTs and for
e mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 181;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and decreation vertexes.
                                                                                                                        Sg
                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                         Chimeric
promoter
                                      polyA_site
                                                                                                                                                  IDNA
                                                                                                                                                                                           promoter
                                                                                                                                                                                                                                   Chimeric
                                                                                                                                                                                                                                                Chimeric
                                                                                                                                                                                                                                                             Chimeric
                                                                                                                                                                                                                                                                                                  Interleukin-12; IL-12; cytokine; growth factor; mouse; plasmid pWRG3169; cancer; tumour; metastasis; gene the cyclic; circular.
                                                                                                                                                                                                                                                                                                                                                          Plasmid
                                                                                                                                                                                                                                                                                                                                                                                     08-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                V02042
                                                                                                                                                                                                                                                                                                                                                                                                                                          V02042 standard; DNA; 7287 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 198 BP; 47 A; 54 C; 51 G; 46 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        891
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||
| gc 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaagctattgcattgaaagcagcaaaggatggagcaaatattgttattgctgcaaagacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aaagctattgcattgaaagcagcaaaggatggagcaaatattgttattgctgcaaagacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aacaccgggaggctggcaggatgtacagtttttatcacaggtgcaagccgtggcattggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tctgctcgccgccgctgtcgccgccacctcctctgatctacgaaagtcatgttaccc
                                                                                                                                                                                                                                                                                                                                                         pWRG3169 encoding
                                                                                                                                                                                                                                    ,
                                                                                                                                                                                                                                                              ı
                                                                                                                                                                                                                                              Mus musculus.
Cytomegalovirus.
Bos taurus.
                                                                                                                                                                                                                                Rhesus macaque polyoma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.0%; ilarity 99.5%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                   /*tag= d
1797..2024
                                                                                                                      /*tag= b
953..1673
                                                                                                                                         /*tag= a
/note= "CMV promoter"
629..810
/note= "bovine
2110..2737
                                                                 1259..1331
                                                                            /product= p35 subunit
/note= "contains an i/
                                                                                                                                                                                                     Location/Qualifiers
                         /*tag=
                                                                                                          /*tag=
                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                         murine interleukin-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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Pred. No. 4.
         growth hormone polyA site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                              an intron'
                                                                                                                                                                                                                                                                                                                metastasis; gene therapy; ds;
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1;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     donor/splicing acceptor is provided between each subunit gene and its CMV promoter. The backbone of the plasmid is from pUC19. pWRG3139 induces at least twice the expression of II-12 as the bicistronic vector pWRG3196 (see VU2043) in vivo and in vitro. A novel method of treating tumours in a mammal involves delivering copies of an expressible foreign genetic construct, especially pWRG3169 or pWRG3196, comprising a promoter operative in the mammalian epidermal cells and DNA sequences encoding p35 and p40 subunits of II-12 to target cells in vivo. Delivery of the construct allows II-12 expression for treatment of solid, metastatic or disseminated tumours, and regression of established tumours. The treatment is effective even when the genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 24-30; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7287 BP; 1798 A; 1877 C; 1846 G; 1766 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                construct containing promoter and sequences encoding interleukin-12 p35 and p40 subunit(s) to target cells in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-041898/04.
P-PSDB; W44004-05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            p35 (see W44004) and p40 (see W44005), of murine interleukin-12 (IL-12). Each subunit gene was cloned from a mouse spleen cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pWRG3169 is a tandem plasmid encoding both subunits, i.e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interleukin-12 gene therapy of tumours - comprises delivering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rakhmilevich AL, Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           construct is delivered to a site distant from the tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library and has been placed under the transcriptional separate cytomegalovirus (CMV) promoter. An SV40 sp
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                                                                                                                             690
                                                                                                                                                                                      565
                                                                                                                                                                                                                                                   630
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                            acttctaggcctgtacggaagtgttacttctgctctaaaagctgcggaattcta
                                                                                                                                                          aggtcccggatccggtggtggtgcaaatcaaagaactgctcctccgtggatgttgccttt 624
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acttctaggcctgtacggaagtgttacttctgctctaaaagctgcggaattgta
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/product= p40 :
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2738..2919
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Best Local
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                                                                                                                                                                                                                                                                                                                                                         protein (GFP) coding sequence. The invention relates to a non-human transgenic animal having a reporter gene coupled to a skin metabolism promoter. The transgenic animal can be used in a method for evaluating a treatment for its effect on skin. The method, together with the transgenic animal are useful for evaluating a compound for its effect on the health or appearance of the skin. The method enables rapid and efficient evaluation of compounds for their effect on skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a construct containing the matrix metalloproteinase 9 (MMP9) promoter linked to the green fluorescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transgenic animal having a reporter gene coupled to a skin metabolism-related promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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MMP9 promoter;
                                                                                                                                                                                                                                                                                                                             Sequence 5068 BP; 1205 A; 1393 C; 1362 G; 1108 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 3; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-395095/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHIS ) SHISEIDO CO LTD.
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993 gccgcaattcccggtcgccaccatggtgagcaagggcgaggagctgt 1039
                685 ctcactatagggwgtcgacccacgcgtccgctcgccgccgccgctgt 731
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Local Similarity 83.3%;
hes 189; Conservative
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green fluorescent protein; skin treatment; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0069945
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                                                                                                                                                                                                                                                   0;
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Search completed: June 12, Job time: 4278 sec

2001, 11:52:00

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Minimum DB
Maximum DB
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Full-length cDNA libraries
Unpublished (2001)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="vector: pcwVSpORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer: Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcWVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
2 others
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                                        GAATTCAAAGAAGAGAAACTGCAGCTGCAACCAAAACCACGTTCTGGTAGCTGTGGAAGA
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Full-length cDNA libraries and normalization
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Contact: Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com" RD 188 g 226 t 5 others
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/lab_host="DH10B"
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/clone="CS0DC029YE05"
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                                                                                                Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Seque Clone distribution: NCI-GAPC clone distribution infor found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lln1.gov/bbrp/image/image.html
Seq primer: -400P from Gibco
High quality sequence stop: 466.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
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National Cancer Institute, Cancer Genome Anal
/organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2772314"
/clone_1ib="NCI_CGAP_Kid11"
/lab_host="DH10B"
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ccacgttctggagctgtggaagaaacatttagaaattgttaaggactctctcagtgatgat 1733
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                                                                                                                                                                                                                      gatgaaaatatcttaaaagaaggaatagaaattttgacgtttatgcaattaaacca 1553
                                                                                                                                                                                                                                                                                                                                                             gctatggatatgctgggaggacctggtatcgaaagccagtgtagaaaagttgatatcatt 1433
                                                                                   GATGAAAATATCTTAAAAGAAGAAGGAATAGAAAATTTTGACGTTTATGCAATTAAACCA
                                                                                                                                                                                                                                                                           GCAGATGCAGCATATTCCAATTTTCCAAAAGCCAAAAAGTTTTACTGGCAACTTTGTCATT
                                                                                                                                                                                                                                                                                         gcagatgcagcatattccattttccaaaagccaaaaagttttactggcaactttgtcatt 1493
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                                                                   GTGGAATCAACTGGTGCTGTTCCAGAATTCAAAGAAGAGAAACTGCAGCTGCAACCAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 963)
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EST.
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National Institutes of Health, Mammalian
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Clone distribution: MGC clone distribution information can
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Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1:
Site_2: Sall; Cloned unidirectionally. Primer:
Average insert size 2 kb. Library constructed
Technologies."
205 c 218 g 238 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 2.2
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; DB 141; Length .2e-94;

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primer: Oligo

Oligo dT. by Life

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BASE COUNT ORIGIN

Query Match Best Local S Matches 662

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u)26904 y1 Sugano mouse kidney mkia Mus
IMAGE:1921110 5' similar to WP:C45B11.3
DEHYDROCENASE ;, mRNA sequence.
AI316248
AI316248.1 GI:4031515
                                                                                                                                                                                                                                                                                                                                                                                          WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL ; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                 Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1996)
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314 286 1810
            /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII (CACCATGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACCTGTGTG, 3' site CACCATGTG). XhoI should
                                                                                                                       /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                  /clone="IMAGE:1921110"
/clone_lib="Sugano mouse
                                                                                                                                                       /sex="female"
                                                                                                                                                                                                  /db_xref="taxon:10090"
                                                                                                                                                                                                              /strain="C57BL"
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                                                                                                                                                              CCATTCACACTGCTGCTATGGATATGCTGGGAGGATCTGGTGTTGAAAACCAATGTAGAA
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158 c 184 g 192 t
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Pred. No. 4.8e-93;
0; Mismatches 99;
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BE893726 602 bp 601436638F1 NIH_MGC_72 mRNA sequence BE893726

Homo sapiens

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
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Tissue Procurement: ATCC/DCTD/DTP
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Contact: Robert Strausberg, Ph.D
Tel: (301) 496-1550
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Mammalla; Eutherla; Primates; Catarrhini;
1 (bases 1 to 602)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
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Pred. No. 6.6e-92;
D; Mismatches 0;
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similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Seq primer: -40UP from Gibco
High quality sequence stop: 416.
Location/Qualifiers
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1 (bases 1 to 620)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Site_2: NotI; Cloned unidirectionally. Primer: Olig
Average insert size 1.69 kb. Life Technologies catal
11549-011"
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Pred. No. 2.3e-90;
0; Mismatches 9;
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 887)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                           cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCMIll5 row: 1 column: 08 High quality sequence stop: 611.
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KEYWORDS SOURCE ORGANISM

Homo human.

sapiens

DEFINITION ACCESSION VERSION

AW966207 54 EST378280 MAGE 1 AW966207 GI:8

541 bp resequences,

MAGI

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01-JUN-2000

RESULT AW966207

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               taaggactctctcagtgatgatgttgttaaagccactcaagcaatctat 1760
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S Hegde,P., Oi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J. and Quackenbush,J. and Assessment of gene expression patterns in a model of cold metastasis using a 19,200 element cDNA microarray Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
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                                                                    tgaacctaaatccagtttggttcaaaccagcactgtgcttataccattgctaagtatggta
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                                                                                                           CATGTATTCCTTATTTGAAAAA-AGCAAAGTTGCTCATATTCTCAATATCAGTCCACCAC
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Plate: 224
541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/dbom=lib="MAGE resequences, MAGI"
/clone_lib="MAGE resequences, MAGI"
/note="Vector: pBluescriptSKm"
110 c 122 g 137 t
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Pred. No. 1.7e-80;
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               agagatgaacagcagatcagtgctgcagtggagaaagccatcaagaaatttggaggaatt 1046
                                                                                                                                                           aatattgttattgctgcaaagaccgcccagccacatccaaaacttctaggcacaatctat 926
AGAGATGAACAGCAAATCAACAGTGCAGTGGAGAAAGCTGTGGAGAAATTTGGAGGAATT
                                                                                                                                           AATATTGTCATTGCTGCGAAGACCACCCAAAAGCACCCGAAACTCCTCGGCACAATCTAC
                                                                                                                                                                                                                  ACAGGTGCAAGCCGAGGCATTGGCAAAGCAATTGCCTTGAAAGCCGCAAAGGATGGAGCC
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BF151259.i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Robert_Strausberg@nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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High quality sequence stop:
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg,
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF151259 675 bp mRNA EST 29-DEC-2000 uz14a11.yl NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3669020 similar to TR:09VB10 Q9VB10 CG5590 PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/strain="C57/B6"
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo d'
Library constructed by Life Technologies. Investigators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  providing samples: Lothar Hennighausen/Robin Humphreys,
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/dev_stage="7 months"
/lab_host="DHIOB"
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Pred. No. 1.2e-79;
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Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Tel; (301) 496-1550

Email: Robert_Strausberg@nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.lnl.gov
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BF182478
BF182478.1 GI:
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601804245F1 NCI_CGAP_Mam5 Mus
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                                                 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1:
Site_2: NotI; Cloned unidirectionally. Primer: Olic
Library constructed by Life Technologies. Investigations
                                                                                                      /clone="IMAGE:4035179"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                                                                                                                     /cryanism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10090"
/clone="Twaco"
                                  providing samples: Lothar Hennighausen/Robin
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IMAGE:4035179
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                                 Humphreys,
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                                                                   AW044841 693 bp mRNA
um14e01.yl Sugano mouse kidney mkia Mus
IMAGE:2192280 5' similar to WP:C45B11.3
DEHYDROGENASE ;, mRNA sequence.
 Eukaryota;
Mammalia;
                    Mus musculus
                                         EST
                                                    AW044841.1
                                house mouse
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Eutheria;
                                                    GI:5905370
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Chordata;
Rodentia;
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Pred. No. 4.1e-79;
""smatches 124;
Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                aaatttggaggaattgatattctggtaaataatgccagtgccattagtttgaccaataca 1091
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                                                                                                                            TTCGGCACAATCTACACGCTGCTGAAGAAATTGAAGCAGCTGGAGGGACGGCCTTGCCT
                                                                                                                                                  ctaggcacaatctatactgctgctgcagaaattgaagcagttggaggaaaggccttgcca
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                                                                                                                                                                                                                                                                     TGCACAGATTTTATCACACGTGCAAGCCGAGGCATTGGCAAAGCAATTGCCTTGAAAGCC
AAATTTGGAGGAATTGATATTTTGGTGAACAATGCCAGTGCTATTAGCTTGACCAACACG
                                                                                                                                                                                                    GCAAAGGATGGAGCCAATATTGTCATTGCTGCGAAGACCACCCAAAAGCACCCGAAACTC
                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 693)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Warra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
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Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer: custom primer used
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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/clone="IMAGE:2192280"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Sugano mouse kidney mkia"
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                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Robert_Strausberg@nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL http://image.lln1.gov plate: LLAM9143 row: e column: 20 High quality sequence stop: 632. Location/Qualiflers
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National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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             /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sa. Site_2: Not1; Cloned unidirectionally. Primer: Oligo Library constructed by Life Technologies. Investigator providing samples: Glibert Smith, NIH"

199 c 224 g 220 t
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/clone_type="tumor, biopsy sample"
/tissue_type="tumor, biopsy sample"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                       /strain-"FVB/N"
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Rodentia;
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Query Match

19.8%;

Score

506.2;

DB 141;

Length 889;

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REFERENCE
AUTHORS
TITLE
JOURNAL
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Mammalia; Eutheria; Rodentia; S
1 (bases 1 to 693)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
Unpublished (1999)
Contact: Robert Strausberg, Ph.
                                                                                                                         mRNA sequence.
BE307752
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601098052F1 NCI_CGAP_Mam5
                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Email: Robert_Strausberg@nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphr.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate: LLAM8549 row: g column: 14

High quality sequence stop: 654.
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/db_xref="taxon:10090"
/clone="IMAGE:3496741"
/clone=lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross t:/dev_stage="7 months"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal. Site_2: Not1; Cloned unidirectionally. Primer: Oligo di Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
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JOURNAL
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Best Local Similarity
Matches 542; Conserv
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                                                       ccagccacatccaaaacttctaggcacaatctatactgctgctgaagaaattgaagcagt 952
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                                                                                                          AGCAATTGCCTTGAAAGCCGCAAAGGATGGAGCCAATATTGTCATTGCTGCGAAGACCAC
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BG245008
BG245008.1 GI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG245008 618 bp mRNA 602358280F1 NCI_CGAP_Mam1 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: Robert_Strausberg@nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 618)
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Plate: LLAM10330 row: p column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Consortium (CLNL) Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
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                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:448915"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                        /note-*Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH*

134 c 156 g 145 t
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Search completed: June 12, 2001, 10:40:35 Job time: 4553 sec

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Result
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     Score
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-08-217-210B-3
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B IDENTIFYING GENES VEL SECRETED OR M P.C. P.C. 2.0 307B 4/020001 4/020001 4/020001 4/020001 4/020001 4/020001 4/020001 4/020001 4/020001	-08-286-740-3 -09-025-09576-3 -09-027-49-68 -09-026-985-68 -09-088-811-15 -08-087-783A-15 -08-194-088B-15 -08-194-088B-15 -08-194-084B-15 -08-444-644-27 -08-444-644-21	-048A-10 -581-3 -581-14 -305A-9 -104A-9
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RESULT 2
US-08-644-664B-6
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APPLICANT: Denney
                          SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll,
                                                                                                                                                                                                                          TITLE OF INVENTION: Gene Amplication Methods NUMBER OF SEQUENCES: 42
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ZIP: 941
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                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                ADDRESSEE: MedLen a constraint Street,
APPLICATION NUMBER: FILING DATE: 01-MAY
                                                                                                                                                CITY: San Francisco
STATE: California
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US-08-761-277A-6
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                                                                                                 Sequence 6, Application US/08761277A Patent No. 5972334 GENERAL INFORMATION:
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                                  APPLICANT: Denney Jr., Dan W.
TITLE OF INVENTION: Vaccines
TITLE OF INVENTION: Leukemia
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
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LENGTH: 633 base pairs
TYPE: nucleic acid
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ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Medlen & Carroll, L
STREET: 220 Montgomery Street,
CITY: San Francisco
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TOPOLOGY: linear
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nilarity 96.1%;
Conservative
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Pred. No. 1.7e-73;
Pred. No. 1.7e-73;
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              Suite
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FILING DATE: 01-MAX-1996
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin.T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: GENITOPE-02406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 633 base pairs
TYPE: nucleic acid
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 598
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             gttttctgttctgcgccgttacagatc 506
                                                                                                   agtogogttotgocgoctcocgoctgtggtgcotcotgaactgcgtcogcogtotaggta 359
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GTTTTCTGTTCTGCGCCGTTACAGATC
                                                                ctcagccggctctccacgctttgcctgaccctgcttgctcaactctacgtctttgtttca 479
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.6%;
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Matches 271
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9045 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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TELEFAX: 212-596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 01 FILING DATE: 19-SEP-1997. ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
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APPLICANT: Sakaguchi,
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                 357
                                             412
                                                                                                237
                                                                                                                                                          Local Similarity
nes 271; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Haley, James F. REGISTRATION NUMBER: 27 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                            LOCATION:
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                                                                                                                                                                                                                                                                                                   NAME/KEY:
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gtaagtttaaagctcaggtcgagaccggggcctttgtccggcgctcccttggagcctacct 416
                                          ttgagtcgcgttctgccgcctcccgcctgtggtgcttctgaactgcgtccgccgtctag 356
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: New York
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Igarashi, Hisanaga
Okumura, Kouichi
                                                                                                                                                          Conservative
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1..757
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8584..8589
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                                                                                                                                                                      10.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27,794
ER: SHGN-12CIP
                                                                                                                                                                    Score 259.4;
Pred. No. 3.1
                                                                                                                                                          Mismatches
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                                                                                                                 Matches 194;
                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Applic Patent No. 5580761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (716) 849-0349 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/739,718
FILING DATE: 29/7/91
APPLICATION NUMBER: 07/156,188
FILING DATE: 16/2/88
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: MS-D
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 720 nucleotide
                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                              IMMEDIATE SOURCE:
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CITY: Buffalo
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELL TYPE:
                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 1
FILING DATE: 23/3/94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States ZIP: 14203-2391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Nelson, M. Bud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCCGGCGCTCCCTTGGAGCCTACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08217210B
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1800 One M&T Plaza
                                                                                                                                                                                                                                                                                                                                                                     720 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilson Greatbatch and John C. Sanford VENTION: Method of Conferring Resistance to VENTION: Immunodeficiency Viral Infection EQUENCES: 27
                                                                                                                 Conservative
                                                                                                                                                                                                                                                           HTLV-I
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                                                                                                                                                                                                                                            virus
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                                                                                                                                                                                                                                                                                         genomic
                                                                                                                            9.78;
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                                                                                                                              Score 249.4; DB 1;
Pred. No. 1.3e-42;
                                                                                                               Mismatches
                                                                                                               6;
                                                                                                                                           Length 720;
                                                                                                               Indels
                                                                                                             1;
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   ; CLONE: Plasmid pSE1 "site binding to HindIII"; CLONE: fragment US-07-920-519-33
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US-07-920-519-33
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

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                                                                                                                                                          TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SALOME, MARK
TITLE OF INVENTION: URATE OXIDASE ACTIVITY PROTEIN,
TITLE OF INVENTION: RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR,
TITLE OF INVENTION: MICRO-ORGANISMS AND TRANSFORMED CELLS
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 16781/276 BEDL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                               MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                 IMMEDIATE SOURCE:
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                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                        NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 22313-0299
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CITY: Alexandria
STATE: Virginia
                                                                                                            STRANDEDNESS:
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                                                                                                                                             LENGTH:
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                                                                                                                           nucleic acid
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                                                                                                                                             422 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LUPKER, JOHANNES LEPLATOIS, PASCUAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GUILLEMOT, JEAN-CLAUDE KAGHAD, MOURAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOISON,
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                                                                                              linear
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US 08-314-586-33

; Sequence 33, Application

; Patent No. 5541098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICATION NUMBER: US 07/659,408
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16781/509/BEDL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LUPKER, JOHANNES
APPLICANT: LEPLATOIS, PASCUAL
APPLICANT: SALOME, MARK
APPLICANT: LAURENT, PATRICK
TITLE OF INVENTION: URATE CAIDASE ACTIVITY PROTEIN,
TITLE OF INVENTION: MICROORGANISMS AND TRANSFORMED CELLS
NUMBER OF SEQUENCES: 40
                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 28-SEP-19
                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, Sui
                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                             CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCTCGCATCTCTCACCCCCCCCCCCCCCCCCTACCTGAGGCCGCCCATCCACGCCGG-T 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KAGHAD, MOURAD
LEGOUX, RICHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GUILLEMOT, JEAN-CLAUDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAPUT, DANIEL
                                                                                                                                                 28-SEP-1994
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85.6%;
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                                                                                                                                                               US/08/314,586
                                                                                                                                                                                                                                                                                                                            Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 181.4; DB Pred. No. 9.3e-29
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                                                                                                                                                                                               Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
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RESULT 8
US-08-371-121-13
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Best Local Similarity 85.6%;
Matches 237; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                 APPLICANT: KAGHAU, ...
APPLICANT: LABIT-LE BOUTEILLER, ...
APPLICANT: LABIT-LE BOUTEILLER, ...
APPLICANT: MAGAZIN, Marilyn
TITLE OF INVENTION: Protein having a cytokine type
TITLE OF INVENTION: activity, recombinant DNA coding for this
TITLE OF INVENTION: transformed cells and microorganisms.
                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                           SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NO (YEHUMIC)
IMMEDIATE SOURCE:
CLONE: Plasmid pSEl "site binding to HindIII"
CLONE: fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 422 base pairs
TYPE: nucleic acid
                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 ggctcgcatctctccttcacgcgcccgccgccctacctgaggccgccatccacgccggtt 298
                                                                                                                                                    CITY: Wa
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CLASSIFICATION:
              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGT 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                                                       20007-5109
                                                                                                                                                                 SEE: FOLEY & LARDNER
3: 3000 K Street, N.W.,
Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08371121
                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                         MINTY, Adrian
                                                                                                                                                                                                                                                                                                                                                        GUILLEMOT, Jean-Claude LEPLATOIS, Pascal
                                                                                                                                                                                                                                                                                                                                                                                        FERRARA, Pascual
                                                                                                                                                                                                                                                                                                                                                                                                        CAPUT,
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                                                          Release #1.0, Version
                              US/08/371,121
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Pred. No. 9.3e-29;
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                                                                                                                                                                                                                                         Patent No. 6001649
GENERAL INFORMATION:
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Best Local Similarity
Matches 237; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 422 base pairs
TYPE: nucleic acid
STRANDEDMESS: double
                                                                                                                                                APPLICANT: CAPUT, Daniel APPLICANT: FERRARA, PASCUAL APPLICANT: MILOUX, Brigitte APPLICANT: MINTY Adrian APPLICANT: VITA, Natalio
                                                                            TITLE OF INVENTION: Protein having a cytokin type
TITLE OF INVENTION: activity, and recombinant DNA, expression vector and
TITLE OF INVENTION: for its preparation.

NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 16781/383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEPAX: (202) 672-5399
TELEX: 904136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: FR 91 00137
                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
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 STREET: King Street Station, Suite 500, 1800 Diagonal STREET: Road, PO Box 299 CITY: ALEXANDRIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 08-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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30-NOV-1992
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Pred. No. 9.3e-29;
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; HYPOTHETICAL: NO
US-07-927-391-14
                                                                                                                                                                                                                                                         US-08-659-206A-1
                                                                                                                                                                                       Sequence 1, Application US/08659206A Patent No. 5922685
GENERAL INFORMATION:
APPLICANT: Rakhmilevich, Alexand
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Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 1678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
ZIP: 53703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                  APPLICANT: Rakhmilevich, Alexander
TITLE OF INVENTION: IL-12 Gene Therapy of Tumors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (703) 683-4109
                                              COUNTRY:
                                                                 CITY: Madison
STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
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CLASSIFICATION:
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OPERATING SYSTEM:
                                                                                                   STREET:
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                                                                                                 ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                GAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gagtcgcgttctgccgcctcccggcttgtggtgcctcctgaactgcgtccgccgtctaggt 358
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                                                   SD
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SYSTEM: PC-DOS/MS-DOS
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Length 422; Indels

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RESULT 11
US-08-893-327-15
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Best Local Similarity
Matches 170; Conserv
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TELEPHONE: 608-251-5000
TELEPAX: 608-251-9166
TELEPAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Seay, Nicholas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Plasmid DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                    625 acttctaggcctgtacggaagtgttacttctgctctaaaagctgcggaattcta 678
                                                                                                                               690
                                                                                                                                                            565
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STRANDENNESS: double
TOPOJOCY
                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
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LOCATION:
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LOCATION: 2983..3990
OTHER INFORMATION: //
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: join(953..1258, 1332..1673)
OTHER INFORMATION: /product= "p35 gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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Application US/08893327
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2110..2737
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4075..4306
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2738..2919
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1797..2024
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Humanized Green Fluorescent Protein Genes and Methods

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; LOCATION:
US-08-893-327-15
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                                                                                                                                                             RESULT
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 6253 base pairs
LENGTH: nucleic acid
TYPE: nucleic acid
                                                                                                        Sequence 17, Application US/08893327 Patent No. 6020192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/588,;
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
NAME: Kitchell, Barbara S.
NAME: Kitchell, Barbara S.
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Best Local Similarity
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                                                                                         GENERAL INFORMATION:
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APPLICANT: Zolotukhin, Sergei APPLICANT: Hauswirth, William W. APPLICANT: Muzyczka, Nicholas TITLE OF INVENTION: Humanized Gr TITLE OF INVENTION: Genes and Me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UFLA:062\KIT
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
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                                                                                                                                                                                                                                                     625
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ZIP: 77210-4433
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(713) 789-2679
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Hauswirth, William W.
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988..1701
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97.1%;
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Genes and
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NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

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ADDRESSEE:

E: Arnold, Whi

White & Durkee

CITY: Houston

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US-08-893-327-17
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CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 08/588,201
APPLICATION NUMBER: US 08/588,201
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kicchell, Barbara S.
REGISTRATION NUMBER: UFLA:062\KIT
                                                                                                                                                                                                                                       Sequence 19, Application US/08893327 Patent No. 6020192
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Best Local Similarity
Matches 169; Conserv
                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (713) 789-2679 INFORMATION FOR SEQ ID NO: 17:
                                                                                                                  APPLICANT: Zolotukhin, Sergei APPLICANT: Hauswirth, William W. APPLICANT: Muzyczka, Nicholas TITLE OF INVENTION: Humanized Gr. TITLE OF INVENTION: Genes and Me
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
   STREET: r. CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 6280 base pair
                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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ZIP: 77210-4433
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TYPE: nucleic acid
STRANDEDNESS: single
COUNTRY:
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                                                                   ADDRESSEE: Arnold,
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US-08-893-327-19
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TELEFAX: (713) 799-2679
INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
LENGTH: 6280 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08659206A Patent No. 5922685
GENERAL INFORMATION:
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Best Local Similarity 97.1%;
Matches 169; Conservative
                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 08/588,201
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            TITLE OF INVENTION: IL-12 Gene Therapy of Tumors NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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REFERENCE/FOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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STATE: WI
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CITY: Madison
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CLASSIFICATION:
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CLASSIFICATION:
                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                   ZIP:
                                                                                                                                                                                  COUNTRY:
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Pred. No. 3.8e-25;
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ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas REGISTRATION NUMBER:

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Best Local Similarity 97.1%;
Matches 169; Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Truscees M. APPLICANT: Wilson, James M. APPLICANT: Fisher, Krishna J. APPLICANT: Fisher. Kn.-Jen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Weitzman, Matthew
TITLE OF INVENTION: Improved Adenovirus Virus
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "plasmid pwRG3196"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Spring House Corporate Cntr, P CITY: Spring House STATE: Pennsylvania
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OTHER INFORMATION: /product= "p35 gen
                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   circular
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Pred. No. 3.8e-25;
D; Mismatches 5;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
FRIGHT: 7852 base pairs
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Best Local Similarity
                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
1704
                                                                  1644 AGGTCCCGGATCCGGTGGTGCAAATCAAAGAACTGCTCCTCAGTGGATGTTGCCTTT 1703
                                                                                                                                        1584 TCGAGGAACTGAAAAACCAGAAAGTTAACTGGTAAGTTTAGTCTTTTTGTCTTTTATTTC 1643
                625 acttctaggcctgtacggaagtgttacttctgctctaaaagctgcggaattcta 678
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                                                                                    aggtcccggatccggtggtggtgcaaatcaaagaactgctcctcagtggatgttgccttt 624
ACTTCTAGGCCTGTACGGAAGTGTTACTTCTGCTCTAAAAGCTGCGGAATTGTA 1757
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97.1%;
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Pred. No. 4.1e-25;
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Search completed: June 12, 2001, 11:36:57 Job time: 5840 sec

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Sequence:
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2561
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gb_pat2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	~ ~	Score	Query Match	Query Match Length DB	DB	ID	Description
		1741.8		3228	9	AX050011	AX050011 Sequence
	N	1659.8	64.8	2764	9	AX050010	AX050010 Sequence
a	ω	602.4		2851	8	AF029260	AF029260 Gallus ga
	4	569		3392	56	AB009864	AB009864 Expressio
	u	556.2		4951		AR073576	AR073576 Sequence
	6	554.2		184684	79	AL162732	AL162732 Homo sapi
ი	7	552.6		215541	65	AC016904	AC016904 Homo sapi
	8	534		8799	56	AF286077	AF286077 Expressio
	9	478		478	9	AX050078	AX050078 Sequence
_	0	432.6		4614	56	AF285183	AF285183 Cloning v
1	1	418.8		1683	89	AK026847	AK026847 Homo sapi

Query Match Best Local Similarity 95.7%; Pred. No. 2.1e-239; Best Local Similarity 95.7%; Pred. No. 2.1e-239; Matches 1767; Conservative 45; Mismatches 7; Indels 28; Gaps 2; Qy 714 gctcgccgccgccgctgtcgccccccctcctctgatctacgaaagtcatgttacccaac 773	SOURCE human. ORGANISM Homo sapiens Dikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE 1 (bases 1 to 3228) AUTHORS Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C. and Clepet, C. TITLE Expression products of genes involved in diseases related to chlesterol metabolism JOURNAL Patent: WO 0071710-A 24 30-NOV-2000; PATTURES Location/Qualifiers Source /organism="Homo sapiens" /db_xref="taxon:9606" BASE COUNT 1077 a 578 c 655 g 910 t 8 others	RESULT 1 AX050011 LOCUS DEFINITION Sequence 24 from Patent W00071710. ACCESSION AX050011 VERSION AX050011 GI:12226384 KEYWORDS	12 400 15.6 633 9 AR016498 13 400 15.6 633 9 AR016498 AR016498 Sequence 14 373 8 14.6 539 10 AX070432 AR096811 Sequence 15 351.4 11.7 1755 88 AK000575 15 315.2 11.3 7155 88 AK000576 A
1734 gttgttaaagccactcaagcaatctatctgtttgaactctccggtgaagatggtggcacg 1	Oy 1494 gatgaaatatcttaaaagaagaatgaatagaaattttgacgtttatgcaattaaacca 1553	gaatttaaaggtgaaattgcagtcaatgcattatggcctaaaacacgccatacacactgct 13	Qy 774 accgggaggctggcaggatgtacagtttttatcacaggtgcaagccgtggcattggcaaa 833

64.8%; Score 1659.8; DB 95.5%; Pred. No. 1e-227;

Length

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RESULT 2
AX050010
LOCUS
DEFINITION
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Sequence 23
AX050010
AX050010.1
                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 2764)
Denefle,P., Rosier Montus,M.F., Arnould-Reguigne,I.,
Clepet,C.
Expression products of genes involved in diseases rel
Cholesterol metabolism
Patent: WO 0071710-A 23 30-NOV-2000;
Aventis Pharma S.A. (FR)
                                                                                                                                                      23 from Patent
       /organism="Homo sapiens"
/db_xref="taxon:9606"
479 c 565 g 80
                                     Location/Qualifiers
                                                                                                                                        GI:12226383
                                                                                                                                                              2764 bp
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WO0071710
        803
                                                                                 Arnould-Reguigne, I., Prades, C.
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                                                                   diseases related
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                                                                                                         Euteleostomi;
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Best Local Similarity
Matches 1685; Conserv
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		Mat	ches	1685; Conservative 45; Mismatches 7; Indels 28; Gaps 2;
•		Qy	796	agtttttatcacaggtgcaagccgtggcattggcaaagctattgcattgaaagcagc
		Db	–	CAGTTTTTATCACAGGTGCAAGCCGTGGCATTGGCAAAGCTATTGCATTGAAAGCAGCAA 60
		Qy	856	ggatggagcaaatattgttattgctgcaaagaccgcccagccacatccaaaacttc
		рь	61	GGAGCAAATATTGTTATTGCTGCAAAGACCGCCCAGCCACATCCAAAACTTCTA
		Qy	916	cacaatctatactgctgctgaagaaattgaagcagttggaggaaaggccttgccat
		дb	121	GCACAATCTATACTGCTGAAGAAATTGAAGCAGTTGGAGGAAAAGGCCTTGCCATGTA 180
			7	
		Dβ	181	TGTTGATGTGAGAGATGAACAGCAGATCAGTGCTGCAGTGGAGAAAGCCATCAAGAAA
	,	y Qy	1036	10
		ф	241	TGGAGGAATTGATATTCTGGTAAATAATGCCAGTGCCATTAGTTTGACCAATACATTG
		Qy	1096	acctaccaagagattggatctgatgatgaacgtgaacaccagaggcacctacct
		Db	301	ACACCTACCAAGAGATTGGATCTGATGAACGTGAACACCAGAGGCACCTACC
		Qy	1156	catctaaagcatgtattccttatttgaaaaagagcaaagttgctcatatcctcaatatca 1215
		Db	361	ATCTAAAGCATGTATTCCTTATTTGAAAAAGAGCAAAGTTGCTCATATCCTCAATATC
		Ÿ	\vdash	
		ğ	4 2 1	TUCACUACTGAACUTAAATCCAGTTTGGTTCAAACAGCACTGTGCTTATACCATH
		γ	7	agtatggtatgtctatgtatgtgcttggaatggcagaagaatttaaaggtgaaattgcag 1335
		ОБ	481	GTATGGTATGTCTATGTATGTGCTTGGAATGGCAGAAGAATTTAAAGGTGAAATTGCA
		У	(u)	tcaatgcattatggcctaaaacagccatacacactgctgctatggatatgctgggaggac 1395
		В	541	CAATGCATTATGGCCTAAAACAGCCATACACACTGCTGCTATGGATATGCTGGGAGGA
		Ÿ	9	<pre>ctggtatcgaaagccagtgtagaaaagttgatatcattgcagatgcagcatattccattt 1455 </pre>
		ō	0	TGGTATCGAAAGCCAGTGTAGAAAAGTTGATATCATTGCAGATGCAGCATATTCCATTT 660
		Qy	1456	tccaaaagccaaaaagttttactggcaactttgtcattgatgaaaatatcttaaaagaag 1515
		рь	661	CCAAAAGCCAAAAAGTTTTACTGGCAACTTTGTCATTGATGAAAATATCTTAAAAGAA
		Qy	1516	aaggaatagaaaattttgacgtttatgcaattaaaccaggtcatcctttgcaaccagatt 1575
		Дb	721	GAATAGAAAATTTTGACGTTTATGCAATTAAACCAGGTCATCCTTTGCAACCAGAT
		Qy	1576	tettettagatgaataceeagaageagttageaagaaagtggaateaaetggtgetgtte 1635
		DЪ	781	CTTCTTAGATGAATACCCAGAAGCAGTTAGCAAGAAAGTGGAATCAACTGGTGCTGTT
		Qy	1636	cagaattcaaagaagagaaactgcagctgcaaccaaaaccacgttctggagctgtggaag 1695
		Ф	841	AATTCAAAGAAGAAACTGCAGCTGCAACCAAAACCACGTTCTGGAGCTGTGGAA
	•	Qy	1696	aaacatttagaattgttaaggactctctcagtgatgatgttgttaaagccactcaagcaa 1755
		В	901	CATTTAGAATTGTTAAGGACTCTCTCAGTGATGATGTTGTTAAAGCCCACTCAAGCA
		Qγ	1756	totatotgtttgaactotocggtgaagatggtggcacgtggtttottgatotgaaaagca 1815
		В	961	CTATCTGTTTGAACTCTCCGGTGAAGATGGTGGCACGTGGTTTCTTGATCTGAAAAGC

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RESULT 3
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Gallus gallus t
AF029260
AF029260.1 GI:
                                                                Archosauria; Aves; Neognathae; Phasianinae; Gallus.
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Piffat, K.A., Ikeda, T.,
Sif, S., Gilmore, T.D. a.
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Piffat, K.A., Ikeda, T.,
Sif, S., Gilmore, T.D. ar
Characterization of the
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Eukaryota; Metazoa;
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; Galliformes;
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        Nehyba,J.,
                                                                                 Vertebrata; Euteleostomi;
mes; Phasianidae;
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        Liss, A.,
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ATATGGTTCAAAAATCACTGTGCCTACACGATTTCTAAATATGGCATGTCCATGTGTGTC
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91; Conservative
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1142. 2791
/gene="relb"
/note="a member of factors"
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RGGRGLRAGRRPPGGPKGAAAAEEMAVPIGAALQDPNVGMAPVUDDLEIIEEVMKEDG
FQPDPPPGSPHDPPKLIPRGLGVVGRRDPFBDPFRLITTQDPKKTGMFFKVECEGR
SAGSILGESSTEASKTLEAIELLNCQAIPEVQVTACLVWKDWPHRVHPHGLVGKDCSN
GLCQVRLQPHANPRHSFSNLGIQCVKKKEIEAAIEKKLQGIDPFKAASLKHNGEVDM
NVVRICFQASYRDGSGRTRGLSPVLSEPIFDKKSTNTSELRICRMNKESGPCTGGEEL
YLLCDKVQKEDIAVVFRKEPWEARADFSQADVHRQGAIVLRTPPYRCVQLSEPVQVEV
FLORLTDRARSRCPYTYLPRENDAYGVKVKRKRGMDDLLEELSGADPYGIEAKRKKP
PPGFMDHFAPLPAADEAFALLADPLDPLSHLDPPSTPQILGRSYFRTPPPTETPTPP
TASWGPICSGGGGTSPRYRPPPTKWGSQWAAPHQ"

865 c 775 g 607 t 3 others
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Location/Qualifiers
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/product="transcription
/protein_id="AAD41539.1"
/db_xref="GI:5305228"
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/db_xref-"taxon:9031"
/tissue_type-"spleen"
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                  Direct Submission

Submitted (16-DEC-1997) to the DDBJ/EMBL/GenBank databases. Su Submitted (16-DEC-1997) to the DDBJ/EMBL/GenBank databases. Su Submitted (16-DEC-1997) to the DDBJ/EMBL/GenBank databases. Su Submitted (19-DEC-1997) submitted (19-
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  and Sugano, S
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                                                                                                              AAGAACTGCTCCTCAGTGAGTGTTGCCTTTACTTCTAGGCCTGTACGGAAGTGTTACTTC
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Homo sapiens chromosome 9 clone RP11-32M23,
PROGRESS ***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McCarthy, S. Anthony, Gearing, D. Paul and Method for identifying genes encoding membrane-associated proteins Patent: US 5952171-A 1 14-SEP-1999;
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On Feb 8, 2001 this sequence version replaced g1:12597074
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AL162732.28 GI:12717974
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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45599 108237: contig of 62639 bp in length
108238 108337: gap of 100 bp
108338 184684: contig of 76347 bp in length
Location/Qualifiers
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                                                                                                                                                                                                                   /note="assembly_fragment:06222
fragment_chain:1"
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fragment_chain:1"
108338 184684
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-70;
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         Indels
                                      Length 184684;
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1900 tttcagggaaactaaaaccaaccaatggcattcatgtcagggaaattgaagattaaaggta 1959

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JOURNAL
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AC016904/c
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                                                Waterston,R.H.
Direct Submission
Submitted (08-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Sep 2, 2000 this sequence version replaced gi:9838138.
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 Center: Washington
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1 (bases 1 to 215541)
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Homo sapiens chromosome 11 clone
SEQUENCE, 14 unordered pieces.
                                                                                                                                                                                Unpublished
                                                                                                                                                                                               The sequence of Homo sapiens
                                                                                                                                                                                                                   Waterston, R.H.
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Genome Center ----
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RP11-307P9,
Sequencing Center
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WORKING DRAFT
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Sequencing vector: plasmid; 15%
Sequencing vector: plasmid; 15%
Chemistry: Dye-primer ET; 85% of reads
Chemistry: Dye-terminator Big Dye; 15% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 204654 bases at least Q40
Consensus quality: 207772 bases at least Q30
Consensus quality: 209589 bases at least Q20
Insert size: 158000; agarose-fp
Insert size: 158000; agarose-fp
Quality coverage: 5.04 in Q20 bases; sum-of-contigs
Quality coverage: 5.07 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: H_NH0307P09
----- Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                       186651
190605
190705
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1577
                                                    vector_side:right"
60722. .104714
                                                                                                                                                             /note="assembly_name:Contig10" 7041. .18594
                clone_end:T7
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                                                                                                                                                                                                    /note="assembly_name:Contig1"
1577. .6940
                                 60722. ...104714
/note="assembly_name:Contig13
                                                                                                                                                                                                                                                                                                                                1. .215541
                                                                                                     /note="assembly_name
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                                                                                                                                                                                                                                                       /clone="RP11-307P9"
                                                                                                                                                                                                                                                                        /chromosome="11"
                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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7040: gap of unknown length
18594: contig of 11554 bp in length
18694: gap of unknown length
60621: contig of 41927 bp in length
60721: gap of unknown length
104714: contig of 4393 bp in length
104814: gap of unknown length
178071: contig of 73257 bp in length
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186650: gap of unknown 1
190604: contig of 3954 t
190704: gap of unknown 1
196770: contig of 6066 t
196870: gap of unknown 1
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27-DEC-2000

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BASE COUNT
ORIGIN
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Best Local Similarity
Matches 579; Conserv
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196871. .202059
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/note="assembly_name:Contig14"
178172. .181556
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39194 c 40592 g 66529 t
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190705. .196770
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184478 . 186550
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181657. .18437
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.184377
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5%; Pred. No. 7.1e-70;
. 45; Mismatches 9;
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Mullins,J.I., Hanley,T., Kafsack,B.F.C
Direct Submission
Submitted (11-JUL-2000) Microbiology,
K-455, Seattle, Washington 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalian cell/vaccinia virus expression vectors with increased stability of retroviral sequences in Escherichia coli: production of feline immunodeficiency virus envelope protein Gene 153 (2), 197-202 (1995)
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1 (bases 1 to 8799)
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/note="synthetic"

2339. .2465

/note="derived from T7"

2474. .2747

/note="derived from P7.5 v.
                                                                                                                                                                                             2777. .3143

/note="murine beta-globin transcriptional regulation unit"

3189 .3851

/note="DHFR"
                                                                                                                                                                                                                                                                                                                                   /note="derived from 2301, 2331
                                                                        4527. .5492
/gene="neomycin resistance"
5496. .5632
/note="derived from SV40 ho
                                                                                                                      4142. .4507
/note="murine beta-globin transcriptional 4527. .5492
                                                                                                                                                                                                                                                                                                                                                                            1917. 1934
/note-"polyhistidine tract"
1960. 2007
/note-"similar to tpa 3' en
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/note="SR-alpha Hybrid Promoter;

SV40 promoter"

1344. .1892
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/db_xref="taxon:146704"
join(1 .500,8708 .8799)
/note="vaccinia thymidine kinase gene
                                            5638. .5911
/gene="thymidine kinase"
                                                                                                                                                                 3888. .4141
/note="derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                          note-"oligopyrimidine tract"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="thymidine kinase"
/note="derived from vaccinia;
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                          note-"derived
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AF286077, complete sequence.
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/note="fl packaging c
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/protein_id="AAG45964.1"
/protein_id="AAG45964.1"
/db_xref=="Gi:12034713"
/translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
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/translation="MSIQHFRVALIPFFAAFCLPVFAHPETLYKKDAGBCDGKBVFYAFLLDKGKTVELCSAAITMSDNTAANLLLTTIGGPKELTAFLHMGDHVTRL
DRWEPELNEAIPNDENDTMBVAMATTLRKLLTGELLTHASRQQLIDWMEADKVAGPL
LRSALPAGWFFADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
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/codon_start=1
/product=""
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6320. .6449
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Sequence 91
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Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 478)
Denefle,P., Rosier-Montus,M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; M
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1. .478
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/db_xref="taxon:9606"
99 c 104 g 12
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    4614 bp
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DNA C11
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     sequence
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AGGCAGAAGTATGCAAAGCATGCATCTC-AATTAGTCAGC-AACCATAGTCCC-GCCCCT 187
                                                                                                                                   502;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cloning vector pSGHV0.
Cloning vector pSGHV0
artificial sequence; v
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/note="multiple cloning complement(3506 ...4366)
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Region: octahistidine tag" 2164. 2205
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join(1038. 1130,1340. 1459,1552. 1716,1969. 2277)
/product="human growth hormone/octahistidine/etch virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="human growth hormone/octahistidine/etch virus protease recognition site fusion protein precursor" /protein_d="AAC598571" /db_xref="GI:12584848"
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/db_xref="taxon:148881"
/db_xref="taxon:148881"
/oin(700. .709,970. .1337)
/oin(700. .709,970. .130.1340. .1459,1552. .1716,1969.
/note="Region: human growth hormone precursor"
/oin(700. .709,970. .1130,1340. .1459,1552. .1716,1969.
                                                                                                                                                                                                                                                                                                                                                 /product="beta-lactamase"
/protein_id="AAG59856.1"
/db_xref="GI:12584847"
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2140. .2163
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RISLLLIQSWLEPYQFLRSYFANSLYYGASDSNYYDLLKDLEEGIQTLMGRLEDGSPR
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1. .4614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Region: tobacco
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2 (bases 1 to 1683)
Sugano, S., Suzuki, Y., Ot
Shibahara, T., Tanaka, T.
                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                  /db_xref="taxon:9606"
                                                                                Location/Qualifiers
                                                 /organism="Homo sapiens"
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Homo sapiens primary epithelial cells of human renal proximal tubule cDNA to mRNA, clone_lib:REC clone:REC00490.
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                                                                                                                                                                                                                                                                                               NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library
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                                                                                                                                                                                                                 University of Tokyo (partly supported by
                                                                                                                                                                                                                                             construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science,
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/cell_type="primary epithelial cells proximal tubule" /clone="REC00490"
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Sequence 6 f
AR016498
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Denney, D.W. Jr.
Gene amplification methods
Patent: US 5776746-A 6 07-JUL-1998;
Location/Qualifiers
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/note="cloning vector
1 333 c 303 g
                                                                                           /organism="unknown"
210 c 155 g
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y Unknown.

M Unknown.

Unclassified.

E 1 (bases 1 to 633)

E 2 (bases 1 to 533)

RS Denney,D.W. Jr.

Vaccines for treatment of lymphoma and leukemia

NAL Patent: US 5972334-A 6 26-OCT-1999;

Location/Qualifiers

1 .633 "...known"

154 t
                                                                                                                                                           tgactaattttttttatttatgcaga-gccgaggccgcctcggcctctgagctattccag
                                                                                                                     aactccgcccatcccgcccctaactccgncccagttccggcccattctccgccccatggc 120
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AAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTCCTCGA------
                                                     TGACTAATTTTTTTTTTATTGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAG
                                                                                                         AACTCCGCCCATCCCGCCCCTAACTCCGCCC--AGTTCCGCCCATTCTCCGCCCCATGGC
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                                                                                                                                                                                                                  al Similarity
487; Conserv
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Pred. No. 5e-48;
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JS 5972334.
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nes 375; Conserv
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                                                                                                                                       atggcctaaaacagccatacacactgctgctatggatatgctgggaggacctggtatcga 1405
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                                                                          AAGCCAGTGTAGAAAAGTTGATATCATTGCAGATGCAGCATATTCCATTTTCCAAAAAGCC
                                                                                                                          ATGGCCTAAAACAGCCATACACACTGCTGCTATGGATATGCTGGGAGGACCTGGTATCGA 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AX070432
Sequence
AX070432
                                                                                                                                                                                                                                                                                                                                                                                                Human genes and gene expression products
Patent: WO 0102568-A 904 11-JAN-2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Klinger,J., Kassam,A., Reinhard,C., Randazzo,F., Kennedy,G.C., Dickson,M., Lamson,G., Drmanac,R., Crkenjakov,R., Drmanac,S., Dickson,M., Labat,I., Leshkowitiz,D., Kita,D., Garcia,V. and Strache-Crain,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates
1 (bases 1 to 390)
Williams, L.T., Escobedo, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AX070432.1
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904 from Patent WO0102568.
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/db_xref="taxon:9606"
68 c 81 g 11:
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                                                                                                                                                                                                                                                                                     Score 373.8;
Pred. No. 2.
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    366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, Virology and Human Genome Center, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (15 FEB-2000) to the DDBJ/EMBL/GenBank databases. Sumio Sugano, Institute of Medical Science, University of Tokyo, Deptment of Virology; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnaldims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 1755)
Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T.,
Shibahara, T., Tanaka, T. and Nakamura, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ranigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M., Ohmori,Y., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S. NEDO human cDNA sequencing project Uppublishad Johans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oligo capping; fis (full insert sequence).
Homo sapiens primary epithelial cells of human rer
tubule cDNA to mRNA, clone_lib:REC clone:REC00542
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Homo sapiens cDNA FLJ20565 fis,
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                                                                                                                                                                                 /protein_id="BAA91263.1"
/db_xref="G1:7020759"
/db_xref="G1:7020759"
/db_xref="G1:7020759"
/tabslation="MSHLAERRRKOKWAVDPONTAWSNDDSKFGORMLEKMGWSKGKG
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SDKKEKSFSLEEKSKISKNRVHYMKFTVGKDLSSKTDLDCIFGKRQSKKTPEGDA
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SDKKEKKSSLEEKSKISKNRVHYMKFTVGKDLSSKEDLSETQVEEKRGKRAKG
KARADAL
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449 c 464 g 352 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="primary proximal tubule"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. .1755
                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                        /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                   note-"cloning vector
                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="REC"
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Score 351.4; DB 88
Pred. No. 4.1e-41;
0; Mismatches 6;
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                                                  1755;
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Search completed: June 12, 2001, 11:40:15 Job time: 7978 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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249	249	305	332	348	418	418	478	1223	1305	Score
9.7										Match
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Ouery Match 51.0%; Score 1305; DB 9; Length 3228; Best Local Similarity 100.0%; Pred. No. 0; Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Oy 714 getegeegeegetgtegegeaceteetetgatetacgaaagteatgttacceaac 773	Eucharyott; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo. REFERENCE 1 (bases 1 to 3228) AUTHORS Denefie, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C. and Clapet, C. TITLE Expression products of genes involved in diseases related to cholesterol metabolism Patent: WO 0071710-A 24 30-NOV-2000; Patent: WO 0071710-A 24 30-NOV-2000; Aventis Pharma S.A. (FR) FEATURES Source /organism-"Homo sapiens" //db_xref-"taxon:9606" BASE COUNT 1077 a 578 c 655 g 910 t 8 others		12 242 9.4 506 58 AB030743 AB030743 Human T-C 142 9.4 508 58 AF014658 AF014658 Human T-C 15 242 9.4 508 58 AF014651 AF014651 Human T-C 16 242 9.4 508 58 AF014661 AF014661 Human T-C 17 242 9.4 502 59 HTU53074 U53074 Human T-CC 18 242 9.4 593 58 AB036353 18 242 9.4 593 58 AB036353 19 242 9.4 755 19 HTU53076 U53076 Human T-CC 21 242 9.4 755 59 HTU5178 22 242 9.4 755 59 HTU5178 23 242 9.4 755 59 HTU5178 24 9.4 755 59 HTU5178 25 242 9.4 755 59 HTU5178 26 242 9.4 755 59 HTU5178 27 242 9.4 757 59 HTY16483 Y16483 Human T-CC 28 242 9.4 757 59 HTY16483 Y16485 Human T-CC 29 242 9.4 757 59 HTY16485 Y16485 Human T-CC 20 242 9.4 757 59 HTY16485 Y16485 Human T-CC 20 242 9.4 757 59 HTY16485 Y16485 Human T-CC 21 242 9.4 757 59 HTY16485 Y16485 Human T-CC 22 242 9.4 757 59 HTY16485 Y16485 Human T-CC 23 242 9.4 757 59 HTY16485 Y16485 Human T-CC 24 9.4 9036 59 HULTOR 25 26 9.4 9036 59 HULTOR 26 9.4 9036 59 HULTOR 27 10 E02504 CDNA encodi 28 9.3 1675 10 E02504 CDNA encodi 29 9.0 1675 10 E02504 CDNA encodi 20 9.1 8.7 407 58 AF228943 HUMAN T-CC 20 10 8.7 441 58 AF228940 AF228943 Human T-CC 21 42 8.7 507 58 AF228944 AF228961 Human T-CC 22 48 8.7 507 58 AF228964 AF228944 Human T-CC 23 AF228944 Human T-CC 24 8.7 507 58 AF228965 AF228945 Human T-CC 25 AF228944 Human T-CC 26 AF228944 Human T-CC 27 59 AF228945 Human T-CC 28 AF228945 HUMAN T-CC 29 Human T-CC 20 AF228944 Human T-CC 20 AF228944 Human T-CC 21 AF228944 Human T-CC 22 AF228944 Human T-CC 23 AF228965 Human T-CC 24 8.7 507 58 AF228965 AF228965 Human T-CC 25 AF228945 Human T-CC 26 AF228945 Human T-CC 27 59 AF228945 Human T-CC 28 AF228945 Human T-CC 29 Human T-CC 20 AF228944 Human T-CC 20 AF228945 Human T-CC 20 AF228945 Human T-CC 21 AF228945 Human T-CC 22 AF228945 Human T-CC 23 AF228945 Human T-CC 24 8.7 507 58 AF228965 AF228965 Human T-CC 25 AF228945 Human T-CC 26 AF228945 Human T-CC 27 AF228945 Human T-CC 28 AF228945 Human T-CC 29 Human T-CC 20 AF228945 Human T-CC 20 A
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2764)
Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.
Clepet, C.
Expression products of genes involved in diseases related to
cholesterol metabolism
Patent: WO 0071710-A 23 30-NOV-2000;
Aventis Pharma S.A. (FR)
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Sequence
AX050078
                                        Clepet,C
                                                                     Eukaryota;
                                                                                Homo sapiens
                                                                                                       AX050078.1
                                                     karyota; Metazoa;
mmalia; Eutheria;
(bases 1 to 478)
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Location/Qualifiers
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cagaattcaaagaagagaaactgcagctgcaaccaaaaccacgttctggagctgtggaag
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Expression products of genes involve cholesterol metabolism Patent: WO 0071710-A 91 30-NOV-2000; Aventis Pharma S.A. (FR)
                                                                                       Denefle, P., Rosier-Montus, M.F.,
                                                                                                                               Chordata;
Primates;
                                                                                                                                                                                                                                                            DNA
WO0071710
                                                       involved
                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                         Arnould-Reguigne, I.,
                                                        in
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 Center project name: bA32M23
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 0% of
                                                                                                                                                      Submitted (06-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 8, 2001 this sequence version replaced g1:12597074.
                                                              Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Informatio
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PROGRESS ***, 3 unordered pieces.
AL162732
Sequencing
                                                                                                                 Center code:
                                                                                                                             Center: Sanger Centre
                                                                                                                                                                                                                                                                                                            Homo sapiens
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 1.8e-252;
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tctgttttaaaattttttagtttttggattgtatactaatgaaaatcttaatgatgtttt
                                                     GTCAGATCAAGCAGTAAAATTAGCTCTTTCAAATCTTCTTGTCATGTAAAATGAAGCTAG
                                                                         gtcagatcaagcagtaaaattagctctttcaaatcttcttgtcatgtaaaatgaaagctag
                                                                                                                             CCCTTTGAGCCTTACATCTCATTCACTGTCTTTCTCCAAGAAAAGTATTTTGGGCGGACA
                                                                                                                                                ccctttgagccttacatctcattcactgtctttctcccaagaaaagtattttgggcggaca
                                                                                                                                                                                                      CATAAGCTTCATTAAGTGGGATTCTAAGACAGTCTGTGTTTTTATATTTCAAGGGTTTAA
                                                                                                                                                                                                                       cataagcttcattaagtgggattctaagacagtctgtgtttttatattttcaagggtttaa
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Insert size: 186775; 9.9% error; agarose-fp
Quality coverage: 13.53x in Q20 bases; sum-of-contigs Quality
coverage: 13.46x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 45498: contig of 45498 bp in length
45499 45598: gap of 100 bp
45599 108237: contig of 62639 bp in length
108238 108337: gap of 100 bp
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ilarity 100.0%;
Conservative
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fragment_chain:1"
108338. .184684
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fragment_chain:1"
45599. .108237
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/db_xref="taxon:9606"
/chromosome="9"
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Pred. No. 5.5e-219;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92209 TCTGTTTTAAAATTTTTAGTTTTTGGATTGTATACTAATGAAAATCTTAATGATGTTTT 92266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13; 85%
Sequencing vector: plasmid; 15%
Sequencing vector: plasmid; 15%
Chemistry: Dye-primer ET; 85% of reads
Chemistry: Dye-terminator Big Dye; 15% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 20454 bases at least Q40
Consensus quality: 207772 bases at least Q30
Consensus quality: 209589 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (08-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens chromosome 11 clo
SEQUENCE, 14 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MO 63108, USA On Sep 2, 2000 this sequence version replaced gi:9838138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality coverage: 5.04 in Q20 bases; agarose-fp Quality coverage: 5.27 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: H_NH0307P09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence of Homo sapiens clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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Insert size: 214241; sum-of-contigs
                                                                                                                                                                                                                                                                                                        consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces
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contig of 5364 bp in length
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              of unknown length
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of unknown length
lg of 3385 bp in length
lg of 3385 bp in length
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104815. .178071
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202160. .208195
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178172. .181556
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208296. .215541
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181657. .184377
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/db_xref="taxon:9606"
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190704: gap of unknown 1
196770: contig of 6066 b
196870: gap of unknown 1
202059: contig of 5189 b
202159: gap of unknown 1
208195: contig of 6036 b
208295: gap of unknown 1
208295: gap of unknown 1
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Pred. No. 5.6e-219;
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Sequence
AX070432
AF285183 4614 bp
Cloning vector pSGHV0,
AF285183
AF285183.1 GI:1258484
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Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J., Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D., Lamson, G., Drmanac, R., Crkenjakov, R., Drmanac, S., Dickson, M., Labat, I., Leshkowitiz, D., Kita, D., Garcia, V. and Strache-Crain, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genes and gene expression products Patent: WO 0102568-A 904 11-JAN-2001; CHIRON CORPORATION (US); HYSEQ, INC. (US LOCALION/Qualifiers
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904 from Patent
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/db_xref="taxon:9606"
68 c 81 g 11
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Pred. No. 1.4e-180;
0; Mismatches 0;
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Cloning vector pSGHV0.
Cloning vector pSGHV0
artificial sequence; vectors.
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1 (bases 1 to 4614)
1 Leahy, D.J., Dann, C.E. III, Longo, P., Perman, B. and A mammalian expression vector for expression and pu secreted proteins for structural studies
Protein Expr. Purif. 20 (3), 500-506 (2000)
20541642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-JUL-2000) Biophysics, Johns Hopkins University, N. Wolfe St., Baltimore, MD 21205, USA mammalian expression vector; directs expression of hGH fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Region:
2164 .2205
/note="Region:
                                                                                                                                                                                                 2233. .2284
/note="multiple cloning site"
complement(3506. .4366)
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join(1038. 1130,1340. 1459,1552. 1716,1969. .2277)
/product="human growth hormone/octahistidine/etch virus
protease recognition site fusion protein"
2140. 2163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="human growth hormone/octahistidine/etch virus protease recognition site fusion protein precursor" /protein_id="AAC59857.1" /db_xref="GI:12584848"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Cloning vector pSGHV0"
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/db_xref="taxon:14881"
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/note="Region: human growth hormone precursor"
/oin(700. .709,970. .1130,1340. .1459,1552. .1:
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Risllligswlbpvqbflsvygasdsnyydlkblbebgiqtlbgsgrlbosps
Tgqifkqtyskfdtnshnddallknygllycfrkdmdkvetflrivqcrsvbgscgfs
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/protein_id="AAG59856.1"
/db_xref="GI:12584847"
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                                  Score 332; DB 56;
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                                                                                                                                                                                                                                                                                                                                                                                                     NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5 - & 3 -end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fuji,Y., Ozaki,K., Hirao,M., Ohmori,Y., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 1683)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AK026847.1 GI:10439802 oligo capping; fis (full insert sequence). Homo sapiens primary epithelial cells of human renal proximal tubule cDNA to mRNA, clone_lib:REC clone:REC00490.
                                                                                                                                                                                                                                                                                                                                                                         Agency).
                                                                                                                                                                                                                                                                                                                                                                                         University of Tokyo (partly supported by Science and Technology
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/clone_lib="REC"
/note="cloning vector p
a 333 c 303 g 5
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                                                                                                                                                                                                                                                        /cell_type="primary
proximal tubule"
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/db_xref="taxon:9606"
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           cgatcgaggggctcgcatctctccttcacgcgcccgccctacctgaggccgccatcc 289
 GAATTC 431
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                                            al Similarity
249; Conserva
                                                                                                                                                                                                                                                                                                                                                                                             AB009864
Expression
AB009864
                                                                                                                                                                                                                                              Submitted (16-DEC-1997) to the DDBJ/EMBL/GenBank databases. Su Sugano, The Institute of Medical Science, University of Tokyo, Department of Virology; 4-6-1, Shirokanedai, Minatoku, Tokyo 1 Japan (E-mail:ssugano@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                      2 (bases 1 to 3392)
Maruyama,K. and Sugano,S.
pME18S-FL3: a versatile expression vector
Published Only in DataBase (1997) In press
Location/Qualifiers
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/plasmid="pME18S-FL3"
/db_xref="taxon:29278"
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 Expression vector AF286077. Expression vector AF286077 artificial sequence; vectors
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McCarthy, S.Anthony, Gearing, D. Paul and Levinson, D. Adam.
Method for identifying genes encoding secreted or
membrane-associated proteins
Patent: US 5952171-A 1 14-SEP-1999;
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Sequence 1 from patent
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Wang,R.F. and Mullins,J.I.
Wang,R.F. and Mullins,J.I.
Mammalian cell/vaccinia virus expression vectors with increased stability of retroviral sequences in Escherichia coli: productic of feline immunodeficiency virus envelope protein Gene 153 (2), 197-202 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (11-JUL-2000) Microbiology, University of Washington, K-455, Seattle, Washington 98195, USA Location/Qualifiers
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Mullins, J.I., Hanley
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                                                /pseudo

5638...6265

/note="vaccinia thymidine k:

6320...6449

/note="similar to pUC19"

6453...7047

/note="p15A intermediate co

7050...8192

/note="similar to pUC19"

complement(7192...8052)
                                                                                                                                                                                                                                  4527. .5492
/gene="neomycin resistance"
5496. .5632
/note="derived from SV40 hormone"
                                                                                                                                                                                                                                                                                   3888. .4141
/note="derived from bovine growth hormone"
4142. .4507
/note="murine beta-globin transcriptional regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /pseudo 502. .8
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/note="DHFR"
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2777. .3143
/note="murine beta-globin transcriptional regulation unit"
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2018. .2288
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/note="polyhistidine tract"
1960. .2007
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/note="SR-alpha
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/db_xref="taxon:146704"
join(1. .500,8708. .8799)
/note="vaccinia thymidine kin
/product="beta lactamase"
/protein_id="AAG45964.1"
/db_xref="GI:12034713"
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/gene="thymidine kinase"
/note="derived from vacc
                                      /codon_start-1
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/note="synthetic"
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/note="derived from
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                                                                                                                                                                                                                  Submitted (21-JUL-1999) to the DDBJ/EMBL/GenBank databases. Hongchuan Li, Kagoshima University, Department of Virology; Sakuragaoka, Kagoshima-city, Kagoshima 890-8520, Japan (E-mail:lhc@med5.kufm.kagoshima-u.ac.jp, Tel:81-99-275-5283,
                                                                                                                                                                                                                                                                                                                                            Li,H., Fujlyoshi,T., Lou,H., Yashiki,S.,
Nunez,L., Munoz,I., Horai,S. and Tajima,K
The presence of ancient HTLV-I provirus [
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human T-cell lymphotropic virus type 1 (isolate:Kagoshima proviral DNA, clone:KAG130.
Human T-cell lymphotropic virus type 1
Viruses; Retroid viruses; Retroviridae; BLV-HTLV retroviru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone: KAG130.
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Human T-cell lymphotropic
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H., Sonoda, S. and Tajima, k.
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8210. .8636
/note="f1 packaging origin"
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                                                                    /proviral
/isolate="Kagoshima HT
/db_xref="taxon:11908"
/clone="KAG130"
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                                                     /note="seropositive"
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Submitted (18-JUL-1997) Institute :
University, Shogoin-Kawahara-Machi
                                                                                                                                                                                                                                                                                                                                                     Jardim, C., Sonoda, S. and Hayami, M. Molecular epidemiology of human T-cell leukemia virus type I (HTLV-1) Brazil: the predominant HTLV-1s in South America differ from HTLV-1s of Japan and Africa, as well as those of Japanese immigrants and their relatives in Brazil
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Yamashita, M., Veronesi, R., Menna-Barreto, M., Harrington, W.J. Jr., Sampio, C., Brites, C., Badaro, R., Andrade-Filho, A.S., Okhura, S., Igarashi, T., Takehisa, J., Miura, T., Chamone, D., Bianchini, O.,
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Human T-cell lymphotropic virus type 1
Viruses; Retroid viruses; Retroviridae;
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Human T-cell lymphotropic virus type 1
Viruses; Retroid viruses; Retroviridae; BLV-HTLV retroviruses.
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1 (bases 1 to 508)
2 Yamashita, M., Veronesi, R., Menna-Barreto, M., Harrington, W.J. Jr., Sampio, C., Brites, C., Baddaro, R., Andrade-Filho, A.S., Okhura, S., Igarashi, T., Takehisa, J., Miura, T., Chamone, D., Blanchini, O., Jardim, C., Sonoda, S. and Hayami, M.
Molecular epidemiology of human T-cell leukemia virus type I (HTLV-1) Brazil: the predominant HTLV-1s in South America differ immigrants and their relatives in Brazil
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Human T-cell lymphotropic virus
terminal repeat sequence.
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University, Shogoin-Kawahara-Machi 53,
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Wiruses: Retroid viruses; Retroviridae; BLV-HTLV retroviruses.

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Yamashita, M., Veronesi, R., Menna-Barreto, M., Harrington, W.J. Jr.,

Sampio, C., Brites, C., Badaro, R., Andrade-Filho, A.S., Okhura, S.,

Igarashit, T., Takehisa, J., Miura, T., Chamone, D., Bianchini, O.,

Jardim, C., Sonoda, S. and Hayami, M.

Molecular epidemiology of human T-cell leukemia virus type I

(HTLV-1) Brazil: the predominant HTLV-1s in South America differ from HTLV-1s of Japan and Africa, as well as those of Japanese immigrants and their relatives in Brazil

Virology 261 (1), 59-69 (1999)

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242; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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173 c
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                                                                                                                                                                                                                                                                    Score 242; DB 58; ]; Pred. No. 6.2e-122; 0; Mismatches 0;
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type 1 isolate BRASP31, 5' lor
                                                                                                                                                                                                                                                                                             Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                      virus type
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Search completed: June 12, Job time: 8889 sec

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Result
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Maximum DB
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/SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
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N92604
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Compugen Ltd
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DNA sequence which Sequence complemen Sequence of the sp HTLV-1 p2lX cDNA. HTLV-1 tax/rex spl SR alpha enhancer/Human T lymphotrop HTLV-1 LTR genomic HTLV-I long termin
                                                                                                                                                                                                                   Description
                                                                                                                                                                 Vector ptraP3 DNA Recombinant DNA ve
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DDP drug resistant	T62780	16	1028		92	45	
bDAT. Bos taurus.	99	13	2640	3.8	98	44	
	634	19	4249		103	43	
₽	Z98741	21	471		104	42	
Promoter region fr	87	21	160		104	41	
EST clone AR253.	V86402	20	304		127	c 40	_
MMP9 promoter GFP	X84027	20	5068		160	39	
Recombinant trans-	T60558	18	36538		163	38	
Shuttle vector pAd	T27558	17	19307	6.4	163	c 37	_
Vgag	T60555	18	12135	6.4	163	36	
cDNA sequence of p	V22139	19	10398	6.4	163	35	
cDNA sequence of p	V22129	19	10398	6.4	163	34	
cDNA sequence of p	V22130	19	10398	6.4	163	3 3	
Ad.AV.CMVLac2 hybr	T15286	17	10398	6.4	163	32	
	Z45253	21	9077	6.4	163	31	
Expression vector	245251	21	9077	6.4	163	30	
Vector containing	V09006	19	9077	6.4	163	29	
tain	V09005	19	9077		163	28	
AV.CMVLacZ cis pla	X33862	20	8509		163	27	
မွ	T59271	18	8509	•	163	26	
Recombinant adenov	T47202	18	8236	6.4	163	25	
4	T27555	17	7897	6.4	163	c 24	_
. Synt	Q30906	13	7892	6.4	163	23	
H H	T27556	17	7852	6.4	163	22	
v	Z39629	21	7612	6.4	163	c 21	_
MMP9 promoter beta	X84028	20	7380	6.4	163	20	
Plasmid pWRG3169 e	V02042	19	7287	•	163	19	
Nucleotide sequenc	Z45931	21	6981		163	18	
Plasmid pwRG3196 e	V02043	19	6295		163	17	
	X08456	20	6280		163	16	
	X08455	20	6280	6.4	163	15	
	X08454	20	6253	6.4	163	14	
Vector plasmid pCM	2783	21	3796	6.4	163	13	
Human secreted pro	\sim	21	198	7.0	179	12	

ALIGNMENTS

V27206;

V27206 standard; cDNA; 4951 BP

Vector ptrAP3 DNA sequence. 12-OCT-1998 (first entry)

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WPI; 1998-312407/27
P-PSDB; W55047.
                                                                                                                                                                      Gearing
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                                                                                                                                                                                                                                                                                                                                                                                                 19-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mat_peptide
                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM BIOTHERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-MAY-1998.
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                                                                                                                                                                            DP,
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/product= human placental alkaline phosphatase
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the DNA sequence of vector ptrAp3. This mammalian expression vector contains a cDNA encoding human placental alkaline phosphatase (AP, see w55047) lacking a signal sequence. When the ptrAp3 is transfected into a mammalian cell line, such as COS7 cells, AP protein is neither expressed nor secreted since the AP cDNA of ptrAp3 does not encode a signal peptide or a membrane coll anchor sequence. However, insertion of a cDNA encoding a signal peptide sequence into ptrAp3 facilitates the expression and secretion of AP upon transfection of the DNA into mammalian cells. The presence of AP activity in the supernatants of transfected cells therefore indicates the presence of a signal sequence in the cDNA of interest. This forms the basis of a novel method for the cDNA of interest. This forms the basis of a novel method for the sequence, i.e. secreted or membrane-associated proteins of potential therapeutic value. An isolated clone (see V27707), designated ethb01016f2, was isolated using the novel method and condess a human neural adhesion protein (see w55045) protein having multiple, consecutive IgG domains. The method is very sensitive automation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 249; Conserv
                                Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying DNA encoding mammalian protein by cloning in reporter gene vector without transforming bacteria and mammalian cells,
                                                                             Chloramphenicol; acetyltransferase;
                                                                                                             Recombinant DNA vector for increased CAT expression
                                                                                                                                              17-MAY-1990
                                                                                                                                                                               N92604;
                                                                                                                                                                                                            N92604 standard;
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                                             Location/Qualifiers
                                                                                                                                            entry)
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Pred. No. 1.3e-105;
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                                                                             vector;
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signal sequence,
and identifying cells
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Matches
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                                            gene expression; regulation;
human T-cell leukaemia; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                            HTLV-I LTR is inserted into pSV-CAT, the U3 region is l region gives 10-100 fold CAT expression. Vector can be in a wide range of animal cells for high levels of expr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTR
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                 Homo sapiens
                                                                         DNA sequence which regulates expression in HTLV and
                                                                                                                                   T42902 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 755 BP; 161 A; 255 C; 178 G; 161 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; ; ; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant DNA vector - c
                                                                                              16-JUN-1997
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/label- R
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/label= U3
                                                                                                                                   DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contains HTLV-I long terminal repeat ligated to dichloramphenicol acetyltransferase activity.
                                                                                                                                                                                                                                                                                                                                                                             Score 242; DB 10
Pred. No. 2.5e-1
0; Mismatches
                                            plasmid; viral infection;
antivirus agent; detectio
                                                                                                                                                                                                                                                                                                                                                                                                10;
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Location/Qualifiers

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Best Local Similarity
Matches 242; Conserv
                                                                                                                                                                                                                                                                                       This sequence represents a DNA molecule with gene expression regulation activity. This sequence is used in a plasmid for regulation of gene expression, and treatment of viral infection pref. human T-cell leukaemia and HIV. The plasmid also encodes a protein which is used as an antivirus agent, and also in a method for detecting cancer. The DNA molecule and protein have potential uses in gene therapy, and the plasmid may also have potential use in the treatment of TSP.
        04-FEB-1992
                       N40080;
                                      N40080 standard;
                                                                                                                                                                                                                                                                                                                                                                          DNA molecule with gene expression regulation activity - for use in e.g. treatment of human T-cell leukaemia and HIV, as antivirus agent
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24-MAR-1995;
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                                                                           477 tc 478
||
592 tc 593
                                                                                                                                                                                                                                                                         Sequence 9045 BP; 2086 A; 3162 C; 1713 G; 2084 T;
                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 38-43; 77pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Igarashi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                  (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-1996;
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95JP-0066559
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8584..8589

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                                       cDNA;
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Best Local Similarity
Matches 242; Conserv
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Diagnosis of human leukaemia and/or lymphoma and virus infection made with part or all of the recombinant DNA. Virus antigenic proteins can be produced. These peptides and proteins, and antibodies against them, are useful for the diagnosis, therapy are prevention of human leukaemia.
                                                                                                                                                                      Viral genomic DNA complementary to RNA of human leukaemia virus useful in recombinant DNA producing therapeutic and diagnostic
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                                                                                                                        Claim 4; Table 1, Page 11-15; 23pp; English
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 Sequence 9047 BP;
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                                                                                                                                                                                                                     WPI; 1984-172336/28.
                                                                                                                                                                                                                                                    Yoshida M,
                                                                                                                                                                                                                                                                                (NICA-) JAPAN FOUND FOR CAN (GANK-) GAN KENKYUKAI ZH. (JURI-) JURIDICAL FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                          11-JUL-1984.
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                                                                                                                                                                                                                                                   Sugano H;
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6834..7130
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 2087 A; 3164 C; 1713 G;
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 2083 T;
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237 ggggctcgcatctctccttcacgcgcccgccgccctacctgaggccgccatccacgccgg 296

9.4%; So ilarity 100.0%; F Conservative 0;

Score 242; DB; Pred. No. 2.2 0; Mismatches

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                                     The present sequence is used in the plasmid vectors of the invention. The vectors which comprise a gene which can induce apoptosis under specific conditions, e.g. guanine phosphoribosyltransferase (gpt)), or a reporter gene, e.g. luciferase, where the gene is situated downstream of a promoter which responds to specific extracellular stimulation such as the presence of a cytokine, e.g. tumour necrosis factor (TNF) or interleukin-1: The vector may be used to transform a suitable cell line, such as a cell line which does not produce hypoxanthine-guanine phosphoribosyl transferase (HGPRT). The transformed cells are used to test the inhibitory effect of a gene or
                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                     Test system for detecting intra-cellular signal transmission inhibition - using vector containing apoptosis-inhibiting or reporter gene and promoter sequence, used for, e.g. screening potential anti-inflammatory agents
                                                                                                                                                                                             Disclosure; Fig 7; 62pp; Japanese.
                                                                                                                                                                                                                                                                                                                    Nagasawa Y,
                                                                                                                                                                                                                                                                                                                                                 (CYTO-) INST CYTOSIGNAL RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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cytokine; tumour necrosis factor; interleukin-1; inhibitory effect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-SEP-1998
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Query Match

9.48;

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241;

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Length 633;

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297

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356

1446

Query Match
Best Local Similarity
Matches 230; Conserv

9.0%; So ilarity 100.0%; I Conservative 0;

Score 230; DB 14; Pred. No. 8.5e-97; 0; Mismatches 0;

Length 1675; Indels

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Sequence 633

BP;

114 A; 210 C; 156

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153 T; 0 other;

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                          (Q50835) shows cDNA prepared from RNA extracted from a HTLV-1 infected cell. This was amplified by PCR and was used to construct p21x cDNA (Q50836). Primers and probes were then manufactured p21x cDNA (Q50836).
Sequence 1675 BP;
                                                                    Claim 1;
                                                                                       Oligo-nucleotide primer - for detecting mRNA of leukemia virus 1 by polymerase chain reaction
                                                                                                                                                                                                                                                                                                                 09-MAY-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                        Q50836 standard; cDNA; 1675
                                                                                                                                         (SHIO ) SHIONOGI & CO
                                                                                                                                                                                  18-DEC-1991;
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                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                detection; splice;
                                                                                                                                                                                                                                                                           HTLV-1;
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                 (Q50837-43), these are useful for the detection of HTLV-1 infection
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                                                                                                                                                                                                                                                                          T cell leukemia virus; PCR; polymerase chain reaction;
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349 A; 613 C;
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other;
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                                                                                                                                                                                                                                                (Q50835) shows cDNA prepared from RNA extracted from a HTLV-1 infected cell. This was amplified by PCR and was used to construct p21x cDNA (Q50836). Primers and probes were then manufactured (Q50837-43), these are useful for the detection of HTLV-1 infection.
                                                                                                                                                                                                                                                                                                                           Oligo-nucleotide primer - for detecting mRNA of human leukemia virus 1 by polymerase chain reaction
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                                                                                                                                                                                                                            Sequence 1866 BP; 394 A; 678 C; 386 G; 408 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection; splice;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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nes 230; Conser
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gtaagtttaaagctcaggtcgagaccgggcctttgtccggcgctcccttggagcctacct 1816
                                                    gtaagtttaaagctcaggtcgagaccgggcctttgtccggcgctcccttggagcctacct 416
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llarity 100.0%;
Conservative (
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                                                                                                                                                                     Gaps
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                                                                                                                                                                                               RESULT
T97159
                                                                                                                           Query Match
Best Local Similarity
                                                                                                                  Matches
                                                                                                                                                                                                                         methods for the expression and co-amplification of genes encoding recombinant proteins in cultured cells. The methods permit the isolation of cell lines which have co-amplified input recombinant sequences which encode an amplifiable marker, one or more expression vectors encoding a protein of interest and optionally a selectable marker. The amplified cells provide large quantities of recombinant proteins suitable for immunotherapy for treatment or lymphomas and leukaemias. The methods permit the production of custom vaccines, including multivalent vaccines that reflect the degree of somatic variation found in a patient's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                            SR alpha enhancer/promoter in plasmid pcDL-SR alpha 296. The SR alpha enhancer/promoter is composed of human T cell leukaemia virus 15' untranslated sequences and the SV40 enhancer. It is reported to increase expression from the SV40 enhancer/promoter by 10-fold in host cells, and is active in a broad range of cell types. The SR alpha enhancer/promoter has been utilised in
                                                                                                                                                                                                                                                                                                                                                                                               expression vectors designed for efficient expression of genes in eukaryotic cells. The invention provides vectors and improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multivalent vaccine to treat B cell lymphoma or leukaemia - comprises at least 2 different recombinant variable regions immunoglobulin molecules derived from B cell lymphoma cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-DEC-1996;
01-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SR alpha enhancer/promoter
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This DNA sequence comprises the HindIII/XhoI fragment of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 104; 177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-549743/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enhancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T97159 standard; DNA; 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENI-) GENITOPE CORP
                                                 359
agtogogttotgoogootcoogootgtggtgcotootgaactgcgtoogoogtotaggta 359
                                                               gctcgcatctctccttcacgcgcccgccgccctacctgaggccgccatccacgccggttg 299
                                              gctcgcatctctccttcacgcgcccgccgccctacctgaggccgccatccacgccggttg 418
                                                                                                                                                                                               633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B-cell malignancy; lymphoma; leukaemia; lification; immunotherapy; therapy; SV40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhesus macaque polyoma virus
Human T cell leukaemia virus
                                                                                                               Conservative
                                                                                                                                                                                            BP; 114 A; 210 C; 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0761277.
96US-0644664.
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                                                                                                                            7.3%;
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                                                                                                             Score 188; DB 18;
Pred. No. 2.5e-77;
0; Mismatches 1;
                                                                                                                                                                                             <u>.</u>
                                                                                                                                                                                               154 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             type
                                                                                                                                             Length 633;
                                                                                                               Indels
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                      with a vector comprising a polynucleotide coding for RNA which is complementary or homologous to a nucleic acid sequence within at least one gene from the retroviral genome and which inhibits replication of the retrovirus. Particularly preferred target genes are those coding for the ENV, POL, GAG proteins. Antisense sequences may also target the ART and TAT splice sites, the region around the translation initiation codon (AUG) or the primer binding site (PBS) of the retrovirus. The method is especially intended to confer resistance to infection by human immunodeficiency virus (HTV), feline leukaemia virus (FeLV) or human T lymphotropic virus 1 (HTLV-1). This sequence is from the long terminal repeat of HTLV-I and represents a target for inhibitory nucleic acid of the
                                                                                                                                                                                                                                                       Conferring resistance to retro-virus infection upon host cells using polynucleotide which directs transcription of RNA which inhibits replication
                                                                                                                                                                                                                                                                                                                                                     Greatbatch W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTLV-1; HTLV-1; LTR; retrovirus; inhibition; resistance; antisense therapy; anti-R; anti-PBS; primer binding site; anti-S; splice site; anti-TAT; anti-ART; anti-GAG; anti-POL; anti-CAP; anti-AUG; translation initiation site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human T lymphotropic virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-OCT-1997
22-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N90825
                                                                                                                                                                                                 To confer retroviral resistance on a cell, the cell is transformed
                                                                                                                                                                                                                                                                                                                                                                                                               16-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human T lymphotropic virus 1 long terminal repeat.
                                                                                                                                                                                                                                                                                                                                                                                 (GREA-) GREATBATCH GEN-AID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N90825
              Invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ctcagccggctctccacgctttgcctgaccctgcttgctcaactctacgtctttgtttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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 revised
                                                                                                                                                                                                                          Fig
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                                                                                                                                                                                                                                                                                                                                                     Sanford
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
449..720
                                                                                                                                                                                                                        3; 43pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
/product= GAG_protein_(part)
/note= "Partial open reading frame only; does not
   include termination codon and initiator Martine include termination codon..."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA;
record which was submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
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                                                                                                                                                                                                                           English.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                  HIV; HTLV-1; FeLV; long terminal repeats; resistance; retroviral infection; infection process; retroviral replication; reverse transcription; translation; retroviral replication; region; primer binding site;
                                              Conferring resistance to retroviral polynucleotide which is transcribed inhibits infection into host cells.
                                                                                                                                                                                                                                                                AUG start codo
                                                                                                                                                                                                                                                                                                                                                                Q68398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                               Disclosure; Fig
                                                                                        WPI; 1994-208683/25
                                                                                                         Greatbatch W,
                                                                                                                                        16-FEB-1988;
29-JUL-1991;
                                                                                                                                                                                                                                               Human lymphotropic virus type
                                                                                                                                                                                                                                                                                                               HTLV-1 LTR genomic fragment.
                                                                                                                                                                                                                                                                                                                                07-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amend
                                                                                                                                                                 16-FEB-1988;
                                                                                                                                                                                                 US5324643-A
                                                                                                                        (GREW
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                                                                                                                                                                                                                                                                                                                                                                                                                                        guaaguuuaaagcucaggucgagaccgggccuuuguccggcgcucccuuggagccuaccu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the sequence and annotations).
                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                         478
                                                                                                                        GREATBATCH GEN-AID LTD
                                                                                R56877
                                                                                                                                                                                                                                                                                                                                                                                                        240
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                                                                                                                                                                                                                                                                codon
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                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP;
                                                                                                         Sanford
                                                                                                                                        88US-0156188.
91US-0739718.
                                                                                                                                                                 88US-0156188
                               ω
                                                                                                                                                                                                                        Location/Qualifiers 452..720
                                                                                                                                                                                                                                                                region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138
                                                                                                                                                                                                                                                                                                                                                                RNA; 720
                              35pp;
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                                                                                                                                                                                                                                                               RNA
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                                                                                                                                                                                                                                                                                                terminal repeats; LTR; target fragments;
                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
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                                                                                                                                                                                                                                                                splice
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                                                        ូ
                                                               infection -
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                                                        anti-sense
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The sequences given in Q68397-99 represent fragments of the HIV, HTLV-1 and FeLV genomes which include the long terminal repeats (LTRs). These sequences were used as target fragments in the me

repeats in the method

and These

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TATABOLT 11
TATABOLT 17
TATABO
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Best Local S
Matches 131
                                                                                                                                                                                                                                                                                                                                  23-MAR-1994;
16-FEB-1988;
29-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the invention. The method confers resistance to retroviral infection upon a host cell by inhibiting at least one step in the infection process, esp. retroviral replication, reverse transcription, and translation. A polynucleotide is introduced into the host cell and transcribed. The polynucleotide is complementary to a region of the retroviral genome selected from the 37-region, the primer binding site, the AUG start codon region and the RNA splice sites. This method can be used to prevent and to treat
                            Disclosure; Column 23-24;
                                                                      Prodn. of cells resistant to transformation in vitro with able to inhibit replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV; human immunodeficiency virus; antisense; replication inhibitor; infection resistant; retrovirus; lymphotropic disease; viral leukaemia; lymphadenopathic; HTLV-I; human T-cell lymphotropic virus type I; AIDS; acquired immune deficiency syndrome; PCR; polymerase chain reaction; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 720
                                                                                                                                                                               WPI; 1997-033571/03
                                                                                                                                                                                                                                    Greatbatch
                                                                                                                                                                                                                                                                                                                                                                                                                                      16-FEB-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTLV-I long terminal repeat region oligonucleotide.
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                                                                                                                                                                                                                                                                                 (GREW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             guaaguuuaaagcucaggucgagaccgggccuuuguccggcgcucccuuggagccuaccu
                                                                                                                                                                                                                                                                                 ) GREATBATCH GEN-AID LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                 Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 138 A; 252 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lymphotropic virus type I.
                                                                                                                                                                                                                                                                                                                                94US-0217210.
88US-0156188.
91US-0739718.
                                                                                                                                                                                                                                 Sanford
                                                                                                                                                                                                                                                                                                                                                                                                                                      88US-0156188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.18;
72.08;
                          29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51;
                                                                                                      DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 182; DB 15;
Pred. No. 1.5e-74;
1; Mismatches 0;
                                                                                                                           retroviral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157
                                                                                                      construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>ი</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 U;
                                                                                                   encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                           bу
                                                                                                   retroviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T47850-T47852 are long terminal repeat (LTR) region polynucleotides of human immunodeficiency virus (HIV), feline immunodeficiency virus (FIV) and human T-cell lymphotropic virus type I (HTLV-I), respectively. Antisense ollgonucleotides against these polynucleotides are used in a method for conferring resistance to retroviral infection on a host cell. The antisense sequences are transfected into the host cell to prevent viral replication by binding to a site important for this process, e.g. the LTR, PBS (primer binding site), R region (essential for the "first jump" of reverse transcription), start codon or certain sites in the 3 and 5 untranslated regions. Resistant cells can be introduced into a patient, e.g. by bone marrow transplant to provide protection against retroviral infection.
                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                        Dumas Milne Edwards J,
                                                                                                                                                                                                                            06-SEP-2000.
                                                                                                                                                                                                                                                     EP1033401-A2
                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                    gene therapy;
                                                                                                                                                                                                                                                                                                                   Human;
                                                                                                                                                                                                                                                                                                                                        Human secreted protein 5' EST,
                                                                                                                                                                                                                                                                                                                                                                  06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                            C08959;
                                                                                                                                                                                                                                                                                                                                                                                                                     C08959 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                  (GEST
                                                                                                                                                                           26-FEB-1999;
                                                                                                                                                                                                   21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      477 tc 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 uugagucgcguucugccgccuccgccuguggugccuccugaacugcguccgccgucuag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gtaagtttaaagctcaggtcgagaccgggcctttgtccggcgctcccttggagcctacct
!:|||:::||||::||||:|||||:|||||||||
                                                                                                  2000-500381/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 guaaguuuaaagcucaggucgagaccgggccuuuguccggcgcucccuuggagccuaccu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131;
                                                                                                                                                                                                                                                                                                                   ń
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 720 BP; 138
                                                                                                                                                                                                                                                                                                                 EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                    ; expressed sequence tag;
chromosome mapping; ss.
                                                                                                                                                                           99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA; 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252
                                                                                                                          Duclert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 182; DB
Pred. No. 1.5e
51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157
                                                                                                                                                                                                                                                                                                                                          SEQ ID
                                                                                                                          P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ç,
                                                                                                                          Giordano
                                                                                                                                                                                                                                                                                                                                          NO: 13034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 U;
                                                                                                                                                                                                                                                                                                                 secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118
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The

present sequence

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one

of a large number of 5'

ESTs derived from

Claim 1; SEQ ID 13034; 71pp + CD-ROM; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
The present sequence is that of eukaryotic expression vector plasmid pCMV-MC1. The plasmid is derived from pCMVbeta by
                                                                                                    New polynucleotide encoding an 
American porcine reproductive
                                                                                                                                                                                Calvert JG,
                                                                                                                                                                                                                                                                                                                                  EP1018557-A2
                                                                                                                                                                                                                                                                                                                                                              Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A27831 standard;
                                        Example 4; Page 43-44; 53pp; English.
                                                                                                                                                                                                             (PFIZ ) PFIZER PROD INC
                                                                                                                                                                                                                                                                                                                                                                                                                     North American PRRS virus; Nidovirales virus; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 198 BP; 47 A; 54 C; 51 G; 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression and secretion vectors.
                                                                                                                                                                                                                                            22-DEC-1998;
                                                                                                                                                                                                                                                                        25-NOV-1999;
                                                                                                                                                                                                                                                                                                      12-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     774
                                                                                       vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 179; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gctattgcattgaaagcagcaaaggatggagcaaatattgttattgctgcaaaagaccgc
                                                                                                                                                   2000-444364/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gctattgcattgaaagcagcaaaggatggagcaaatattgttattgctgcaaagaccgc 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           accgggaggctggcaggatgtacagtttttatcacaggtgcaagccgtggcattggcaaa 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            accgggaggctggcaggatgtacagtttttatcacaggtgcaagccgtggcattggcaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasmid
                                                                                       'n
                                                                                                                                                                                                                                                                                                                                                              Porcine reproductive and respiratory syndrome virus. Human cytomegalovirus.
                                                                                                                                                                                Welch SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                       protecting
                                                                                                                                                                                                                                         98US-0113345
                                                                                                                                                                                                                                                                        99EP-0309409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCMV-MC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 3796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                      swine
                                                                                                                                                                               Sheppard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
                                                                                    an infectious RNA molecule of a North
ve and respiratory syndrome virus for one and other animals from infection by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 179; DB; Pred. No. 4e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                ಕ್ಷ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21; Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        swine; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                       use
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X08454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytomegalovirus (CMV) immediate early promoter was accomplished by substituting the sequence between SacI and the 2nd NotI site of CPCMV-MC1 with a synthetic linker. North American porcine reproductive and respiratory syndrome (PRRS) virus P129A cDNA (see A27809) was cloned into the modified vector to create pcMV-S-P129 (ATCC 203489), which was used to demonstrate cellular expression of PRRS virus by direct transfection of cDNA into cells. The invention relates to polynuclectide molecules, plasmids, viral vectors and transfected host cells that comprise North American PRRS DNA. It also relates to polynucleotide molecules, viral vectors and transfected host cells encoding a genetically modified North American PRRS virus that is disabled in its ability to cause PRRS, or which encodes 1 or more heterologous antigenic epitopes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                          humanisation; reporter gene; substrate; cofactor; firefly luciferase; alkaline phosphatase; chloramphenicol acetyltransferase; CAT; beta glucu
                                                                                                                                                                                                                                                                                                                                                                    Green fluorescent protein; gfp; jellyfish;
                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUN-1999
            WPI; 1999-132241/11
                                      Hauswirth W,
                                                                                                  16-JUL-1997;
                                                                                                                                                                                          WO9903997-A1.
                                                                                                                                                                                                                                                                                                                                                                                                   AAV vector sequence comprising humanised green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X08454 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3796 BP; 953 A; 934 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replacing the LacZ coding sequence with a linker containing multiple restriction sites. Modification of the human
                                                                  (UYFL ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     513 ctgaaaaaccagaaagttaactggtaagtttagtcttttttgtcttttatttcaggtcccg 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for use as a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gcctgtacggaagtgttacttctgctctaaaagctgcggaatt 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gatccggtggtggtgcaaatcaaagaactgctcctcagtggatgttgcctttacttctag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctgaaaaaccagaaagttaactggtaagtttagtctttttgtcttttatttcaggtcccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gcctgtacggaagtgttacttctgctctaaaagctgcggaatt 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gatccggtggtggtgcaaatcaaagaactgctcctcagtggatgttgcctttacttctag
W96328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                    FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                        Muzyczka
                                                                                                  97US-0893327
                                                                                                                                 98WO-US14692
                                                                                                                                                                                                                                                    Location/Qualifiers 988..1704
                                                                                                                                                                                                                      /*tag= a
/product= "Humanised green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.48;
                                          z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                          Zolotukhin

 Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 163; DB 21; pred. No. 8.7e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        956 G; 953 T;
                                                                                                                                                                                                                      fluorescent protein"
                                                                                                                                                                                                                                                                                                                                                                       Aequorea
                                                                                                                                                                                                                                                                                                                             glucuronidase; GUS; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0 other;
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                                                                                                                                                                                                                                                                                                                                                                          victoria;
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RESULT 15
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identify transformed cells, to measure gene expression in vitro and in vivo, to label specific cells in multicellular organisms (e.g. to study cell lineage's), to label and locate fusion proteins, and to study intracellular trafficking. Commonly used reporter genes include beta-galactosidase, firefly luciferase, alkaline phosphatase; chloramphenicol acetyltransferase (CAT), and beta glucuronidase (GUS). However, these have limitations in their use. Frequently, these reporter genes require the addition of a substrate and the size of certain proteins means that the expression of reporter fusion proteins means that the expression of reporter fusion proteins can be difficult. The light stimulated Grp
                                                                                                                                                                                                                                                           Green fluorescent protein; gfp; jellyfish; Aequorea victoria; humanisation; reporter gene; substrate; cofactor; beta galact firefly luciferase; alkaline phosphatase; chloramphenicol acetyltransferase; CAT; beta glucuronidase; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fluorescence is species independent and does not require any cofactors substrates or additional gene products from Aequorea victoria an as the GFP genes have been humanised, they are expressed at sufficient levels to be detectable in human cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised green fluorescent protein (gfp) genes can be used to identify transformed cells, to measure gene expression in vitro and
                                                                                                                                                                                                                                                                                                                                           AAV vector sequence comprising humanised green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                             28-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   X08455 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unlike previous GFP proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanised green fluorescent protein expression and identify transformed
             16-JUL-1997;
                                             16-JUL-1998;
                                                                            28-JAN-1999
                                                                                                             WO9903997-A1
                                                                                                                                                                                                                             Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gatccggtggtggtgcaaatcaaagaactgctcctcagtggatgttgcctttacttctag 632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
            97US-0893327
                                             98WO-US14692
                                                                                                                                                                           Location/Qualifiers 988..1731
                                                                                                                                          /product= "Humanised green fluorescent protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
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Pred. No. 8.4e-66;
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                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                  Sequence 6280 BP; 1515 A; 1627
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                                          633
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                gcctgtacggaagtgttacttctgctctaaaagctgcggaatt 675
                                                                                                gatccggtggtggtgcaaatcaaagaactgctcctcagtggatgttgcctttacttctag 632
                                                                                                                                                         ctgaaaaaccagaaagttaactggtaagtttagtcttttttgtcttttatttcaggtcccg 863
                                                                                                                                                                           ctgaaaaaccagaaagttaactggtaagtttagtctttttgtcttttatttcaggtcccg 572
gcctgtacggaagtgttacttctgctctaaaagctgcggaatt 966
                                                                            gatccggtggtgcaaatcaaagaactgctcctcagtggatgttgcctttacttctag
                                                                                                                                                                                                                                       163;
                                                                                                                                                                                                                                 6.4%; Score 163; DB 20; ilarity 100.0%; Pred. No. 8.4e-66; Conservative 0; Mismatches 0;
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Search completed: June Job time: 5905 sec 12, 2001, 14:19:58

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RESULT 14
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Best Local
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                                                                                                                                                  CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 386)
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                                                                                     www-bio.llni.gov/bbrp/image/image.html
Insert Length: 937 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 342.
                                                                                                                                                                                                                                                           Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similar to
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64 c 89 g 172 t 7 others
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1130551"
                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386 bp mRNA EST 21-OCT-1997 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130551 WP:C17G10.8 CE02490 ALCOHOL DEHYDROGENASE;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:2526864
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Pred. No. 4.2e-161;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 GACTACTGATGACTTTGTAAAAATGTTTTCAGGGAAACTAAAACCAACAATGGCATTCAT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gtcagggaaattgaagattaaaggtaacatggccctagcaatcaaattggagaagctaat 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gactactgatgactttgtaaaaatgttttcagggaaactaaaaccaacaatggcattcat 1933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCAGGGAAATTGAAGATTAAAGGTAACATGGCCCTAGCAATCAAATTGGAGAAGCTAAT
                                 Genexpress Genethon
Genethon Centre de recherche sur le Genome
1, rue de l'Internationale, BP60 91002 EVRY
                                                                                                                                                                        Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell, H., Marlage-Samson,R., Pletu,G., Pouliot,Y., Sebastiani-Kabaktchis,C. and Tessier,A.

IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                         Z19446 340 bp mRNA EST 10-FEB-1993
HSB28F112 STRATAGENE Human skeletal muscle cDNA library, cat.
#936213. Homo sapiens cDNA clone 28F11, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                           EST.
                                                                                                 Contact: Genethon
                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                         Acad.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="NCI_CGAP_Br2"
                                                                                                                                       Sci. III,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.7%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 325; DB 9; Logical Pred. No. 1.4e-160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                       Sci. Vie
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                                                                                                                                       318
                                                                                                                                       (2),
                                                                                                                                       263-272 (1995)
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                                     Humain
Cedex,
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